

STN Columbus

* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	NOV 21	CAS patent coverage to include exemplified prophetic substances identified in English-, French-, German-, and Japanese-language basic patents from 2004-present
NEWS	3	NOV 26	MARPAT enhanced with FSORT command
NEWS	4	NOV 26	CHEMSAFE now available on STN Easy
NEWS	5	NOV 26	Two new SET commands increase convenience of STN searching
NEWS	6	DEC 01	ChemPort single article sales feature unavailable
NEWS	7	DEC 12	GBFULL now offers single source for full-text coverage of complete UK patent families
NEWS	8	DEC 17	Fifty-one pharmaceutical ingredients added to PS
NEWS	9	JAN 06	The retention policy for unread STNmail messages will change in 2009 for STN-Columbus and STN-Tokyo
NEWS	10	JAN 07	WPIDS, WPINDEX, and WPIX enhanced Japanese Patent Classification Data
NEWS	11	FEB 02	Simultaneous left and right truncation (SLART) added for CERAB, COMPUAB, ELCOM, and SOLIDSTATE
NEWS	12	FEB 02	GENBANK enhanced with SET PLURALS and SET SPELLING
NEWS	13	FEB 06	Patent sequence location (PSL) data added to USGENE
NEWS	14	FEB 10	COMPENDEX reloaded and enhanced
NEWS	15	FEB 11	WTEXTILES reloaded and enhanced
NEWS	16	FEB 19	New patent-examiner citations in 300,000 CA/CAPLUS patent records provide insights into related prior art
NEWS	17	FEB 19	Increase the precision of your patent queries -- use terms from the IPC Thesaurus, Version 2009.01
NEWS	18	FEB 23	Several formats for image display and print options discontinued in USPATFULL and USPAT2
NEWS	19	FEB 23	MEDLINE now offers more precise author group fields and 2009 MeSH terms
NEWS	20	FEB 23	TOXCENTER updates mirror those of MEDLINE - more precise author group fields and 2009 MeSH terms
NEWS	21	FEB 23	Three million new patent records blast AEROSPACE into STN patent clusters
NEWS	22	FEB 25	USGENE enhanced with patent family and legal status display data from INPADOCDB
NEWS	23	MAR 06	INPADOCDB and INPAFAMDB enhanced with new display formats
NEWS	24	MAR 11	EPFULL backfile enhanced with additional full-text applications and grants
NEWS	25	MAR 11	ESBIOBASE reloaded and enhanced
NEWS EXPRESS	JUNE 27 08		CURRENT WINDOWS VERSION IS V8.3, AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.
NEWS HOURS			STN Operating Hours Plus Help Desk Availability
NEWS LOGIN			Welcome Banner and News Items
NEWS IPC8			For general information regarding STN implementation of IPC 8

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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 09:34:22 ON 12 MAR 2009

=> file medline

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

FULL ESTIMATED COST

ENTRY

SESSION

0.22

0.22

FILE 'MEDLINE' ENTERED AT 09:34:30 ON 12 MAR 2009

FILE LAST UPDATED: 11 Mar 2009 (20090311/UP). FILE COVERS 1949 TO DATE.

MEDLINE and LMEDLINE have been updated with the 2009 Medical Subject Headings (MeSH) vocabulary and tree numbers from the U.S. National Library of Medicine (NLM). Additional information is available at

http://www.nlm.nih.gov/pubs/techbull/nd08/nd08_medline_data_changes_2009.html.

On February 21, 2009, MEDLINE was reloaded. See HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

See HELP RANGE before carrying out any RANGE search.

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713700 STRUCTURE

274517 STRUCTURES

900857 STRUCTURE

(STRUCTURE OR STRUCTURES)

35628 ARCHITECTURE

3423 ARCHITECTURES

38295 ARCHITECTURE

(ARCHITECTURE OR ARCHITECTURES)

43688 OBJECT

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60507 OBJECT

(OBJECT OR OBJECTS)

1958 DOI

671 DOIS

2624 DOI

(DOI OR DOIS)

397 URI

134 URIS

452 URI

(URI OR URIS)

105 URN

15 URNS

110 URN

(URN OR URNS)

481 ARK

14 ARKS

491 ARK

(ARK OR ARKS)

47 PURL

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48 PURL

(PURL OR PURLS)

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4 LSIDS

6 LSID

(LSID OR LSIDS)

8 GUID

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=> d bib an 1-6
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L2 ANSWER 1 OF 6 MEDLINE on SIN
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Full Text
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AN 2008661253 MEDLINE
DN PubMed ID: 18692976
TI The All-Species Living Tree project: a 16S rRNA-based phylogenetic tree of
all sequenced type strains.
AU Yaza Pablo; Richter Michael; Peplies Jorg; Euzebey Jean; Amann Rudolf;
Schleifer Karl-Heinz; Ludwig Wolfgang; Glockner Frank Oliver;
Rossello-Mora Ramon
CS Marine Microbiology Group, Institut Mediterrani d'Estudis Avancats
(CSIC-UIB), C/ Miquel Marqués 21, E-07190 Esporles, Illes Balears,
Mallorca, Spain.
SO Systematic and applied microbiology, (2008 Sep) Vol. 31, No. 4, pp.
241-50. Electronic Publication: 2008-08-09.
Journal code: 8306133. ISSN: 0723-2020.
CY Germany: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200812
ED Entered SIN: 17 Oct 2008
Last Updated on SIN: 2 Jan 2009
Entered Medline: 16 Dec 2008
AN 2008661253 MEDLINE
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L2 ANSWER 2 OF 6 MEDLINE on SIN
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Full Text
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AN 2008508769 MEDLINE
DN PubMed ID: 18689813
TI Inter-species normalization of gene mentions with GNAT.
AU Hakenberg Jorg; Flake Conrad; Leaman Robert; Schroeder Michael; Gonzalez
Graciela
CS Department of Computer Science and Engineering, Arizona State University,
Tempe, AZ 85287, USA.. joerg.hakenberg@asu.edu
SO Bioinformatics (Oxford, England), (2008 Aug 15) Vol. 24, No. 16, pp.
1126-132.
Journal code: 9808944. E-ISSN: 1460-2059.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200810
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ED Entered STN: 12 Aug 2008
 Last Updated on STN: 21 Oct 2008
 Entered Medline: 20 Oct 2008
 AN 2008508769 MEDLINE

L2 ANSWER 3 OF 6 MEDLINE on STN
Full Text
 AN 2007193000 MEDLINE
 DN PubMed ID: 17394580
 TI Children's questions: a mechanism for cognitive development.
 AU Chouinard Michael M
 CS Department of SSHA, University of California, Merced, CA 95344, USA..
mchouinard@ucmerced.edu
 SO Monographs of the Society for Research in Child Development, (2007) Vol.
 72, No. 1, pp. vii-ix, 1-112; discussion 113-26.
 Journal code: 7508397. ISSN: 0037-976X.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, N.I.H., EXTRAMURAL)
 LA English
 FS Priority Journals
 EM 200706
 ED Entered STN: 31 Mar 2007
 Last Updated on STN: 28 Jun 2007
 Entered Medline: 27 Jun 2007
 AN 2007193000 MEDLINE

L2 ANSWER 4 OF 6 MEDLINE on STN
Full Text
 AN 2007050471 MEDLINE
 DN PubMed ID: 17254295
 TI NERBio: using selected word conjunctions, term normalization, and global
 patterns to improve biomedical named **entity** recognition.
 AU Tsai Richard Tzong-Han; Sung Cheng-Lung; Dai Hong-Jie; Hung Hsieh-Chuan;
 Sung Ting-Yi; Hsu Wen-Lian
 CS Institute of Information Science, Academia Sinica, Nankang, Taipei 115,
 Taiwan, Republic of China.. htsai@iis.sinica.edu.tw
 SO BMC bioinformatics, (2006) Vol. 7 Suppl 5, pp. S11. Electronic
 Publication: 2006-12-18.
 Journal code: 100965194. E-ISSN: 1471-2105.
 Report No.: NLM-PMC1764467.
 CY England: United Kingdom
 DT (EVALUATION STUDIES)
 Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)
 LA English
 FS Priority Journals
 EM 200704
 ED Entered STN: 27 Jan 2007
 Last Updated on STN: 27 Apr 2007
 Entered Medline: 26 Apr 2007
 AN 2007050471 MEDLINE

L2 ANSWER 5 OF 6 MEDLINE on STN
Full Text
 AN 2005695098 MEDLINE
 DN PubMed ID: 16382832
 TI The Microbial Rosetta Stone database: A common **structure** for microbial
 biosecurity threat agents.
 AU Ecke David J; Sampath Rangarajan; Willett Paul; Samant Vivek; Massire
 Christian; Hall Thomas A; Hari Kumar; McNeil John A; Buchen-Osmond
 Cornelia; Budowle Bruce
 CS Ibis Division of Isis Pharmaceuticals, 1891 Rutherford Rd., Carlsbad, CA
 92008, USA.
 SO Journal of forensic sciences, (2005 Nov) Vol. 50, No. 6, pp. 1380-5.
 Journal code: 0375370. ISSN: 0022-1198.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
 LA English
 FS Priority Journals
 EM 200602

ED Entered STN: 31 Dec 2005
Last Updated on STN: 8 Feb 2006
Entered Medline: 7 Feb 2006
AN 2005695098 MEDLINE

L2 ANSWER 6 OF 6 MEDLINE on STN

Full Text

AN 2004531610 MEDLINE
DN PubMed ID: 15502395
TI A new mechanosensitive channel SAKCA and a new MS channel blocker GsTMx-4.
AU Sokabe Masahiro; Naruse Keiji; Qiong-Yao Tang
CS Department of Physiology, Nagoya University Graduate School of Medicine.
SO Nippon yakurigaku zasshi. Folia pharmacologica Japonica, (2004 Nov) Vol. 124, No. 5, pp. 301-10. Ref: 40
Journal code: 0420550. ISSN: 0015-5691.
CY Japan
DT (ENGLISH ABSTRACT)
(IN VITRO)
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LA Japanese
FS Priority Journals
EM 200502
ED Entered STN: 26 Oct 2004
Last Updated on STN: 1 Mar 2005
Entered Medline: 25 Feb 2005
AN 2004531610 MEDLINE

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316 METADATA
713700 STRUCTURE
274517 STRUCTURES
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AND (STRUCTURE OR ARCHITECTURE OR OBJECT)

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L4 5 L3 NOT L2

=> d bib ab 1-5

L4 ANSWER 1 OF 5 MEDLINE on STN

Full Text

AN 2008664110 MEDLINE
DN PubMed ID: 18675585
TI Analysis of the internal transcribed spacer 2 (ITS2) region of
scuticociliates and related taxa (Ciliophora, Oligohymenophorea) to infer
their evolution and phylogeny.
AU Miao Miao; Warren Alan; Song Weibo; Wang Shi; Shang Huimin; Chen Ziqui
CS Laboratory of Protozoology, Ocean University of China, Qingdao 266003,
China.

SO Protist, (2008 Oct) Vol. 159, No. 4, pp. 519-33.
 Journal code: 9806488. ISSN: 1434-4610.

CY Germany: Germany, Federal Republic of

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200812

ED Entered STN: 18 Oct 2008
 Last Updated on STN: 2 Jan 2009
 Entered Medline: 16 Dec 2008

AB The ITS2 (ITS--internal transcribed spacer) region of the rDNA in 11 representative scuticociliates and two **ambiguously** related genera was analyzed. In common with other eukaryotes, the putative ITS2 folding pattern consists of a closed loop with four helices supported by minimum free energy and compensatory base changes (CBCs), although two of these helices are variable and sometimes absent. Three topologies were obtained on the basis of traditional primary sequence analysis, "string" strategy of secondary **structure** and analysis of the combined data. It was found that the secondary **structure** information could help to improve alignment and utilize appropriately phylogenetic strategies. The proposed phylogenies, though differing between sequence- and **structure**-based results, provide consistent support for high-level clades: the systematically questionable genera Dextotrichides and Cardiostomatella always cluster together in a clade basal to the scuticociliates s.s., whereas Pleuronema branches from other uronematids at a deep level, and is hence a divergent **taxon**. Within the well-supported monophyletic philasterids, a sister relationship exists between Orchitophrya and Mesanophrys, while Uronema shows a close relationship with the group including Paranophrys and Parauronema. The positions of Metanophrys, Pseudocohnilembus and Anophryoides among the philasterids remain poorly **resolved**. Our findings firmly support the proposed evolutionary scenario inferred previously both from morphological and molecular data.

L4 ANSWER 2 OF 5 MEDLINE on STN

Full Text

AN 2008532719 MEDLINE

DN PubMed ID: 18655698

TI ITS2 data corroborate a monophyletic chlorophycean DO-group (Sphaeropleales).

AU Keller Alexander; Schleicher Tina; Forster Frank; Ruderisch Benjamin; Dandekar Thomas; Muller Tobias; Wolf Matthias

CS Department of Bioinformatics, University of Wurzburg, Am Hubland, 97074 Wurzburg, Germany.. a.keller@biozentrum.uni-wuerzburg.de

SO BMC evolutionary biology, (2008) Vol. 8, pp. 218. Electronic Publication: 2008-07-25.
 Journal code: 100966975. E-ISSN: 1471-2148.
 Report No.: NLM-PMC2519086.

CY England: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)
 (RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals

EM 200809

ED Entered STN: 26 Aug 2008
 Last Updated on STN: 18 Sep 2008
 Entered Medline: 17 Sep 2008

AB BACKGROUND: Within Chlorophyceae the ITS2 secondary **structure** shows an unbranched helix I, except for the 'Hydrodictyon' and the 'Scenedesmus' clade having a ramified first helix. The latter two are classified within the Sphaeropleales, characterised by directly opposed basal bodies in their flagellar apparatuses (DO-group). Previous studies could not **resolve** the **taxonomic** position of the 'Sphaeroplea' clade within the Chlorophyceae without **ambiguity** and two pivotal questions remain open: (1) Is the DO-group monophyletic and (2) is a branched helix I an apomorphic feature of the DO-group? In the present study we analysed the secondary **structure** of three newly obtained ITS2 sequences classified within the 'Sphaeroplea' clade and **resolved** sphaeroplealean relationships by applying different phylogenetic approaches based on a combined sequence-**structure** alignment. RESULTS: The newly obtained ITS2 sequences of Ankyra judayi, Atractomorpha porcata and Sphaeroplea annulina of the 'Sphaeroplea' clade do not show any branching in the secondary **structure** of their helix I. All applied phylogenetic methods highly

support the 'Sphaeroplea' clade as a sister group to the 'core Sphaeropleales'. Thus, the DO-group is monophyletic. Furthermore, based on characteristics in the sequence-**structure** alignment one is able to distinguish distinct lineages within the green algae. CONCLUSION: In green algae, a branched helix I in the secondary **structure** of the ITS2 evolves past the 'Sphaeroplea' clade. A branched helix I is an apomorphy characteristic within the monophyletic DO-group. Our results corroborate the fundamental relevance of including the secondary **structure** in sequence analysis and phylogenetics.

L4 ANSWER 3 OF 5 MEDLINE on STN

Full Text

AN 2002164747 MEDLINE

DN PubMed ID: 11846600

TI Using the volumetric indices of telencephalic **structures** to distinguish Salamandridae and Plethodontidae: comparison of three statistical methods.

AU Dore Jean-Christophe; Ojasoo Tiit; Thireau Michel

CS Laboratoire des Substances Naturelles, ESA 8041 CNRS, Museum national d'Histoire naturelle, 63 rue Buffon, 75005 Paris, France.. dore@mnhn.fr

SO Journal of theoretical biology, (2002 Feb 7) Vol. 214, No. 3, pp. 427-39. Journal code: 0376342. ISSN: 0022-5193.

CY England: United Kingdom

DT (COMPARATIVE STUDY)

Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200204

ED Entered STN: 19 Mar 2002

Last Updated on STN: 20 Apr 2002

Entered Medline: 19 Apr 2002

AB The aim of this study was to establish whether appropriate statistical analysis of 16 volumetric indices corresponding to 16 **structures** making up the entire telencephalon of Urodela could distinguish between two families, Salamandridae and Plethodontidae. We compared the efficiency of three statistical methods (stepwise discriminant analysis, artificial neural networks, correspondence factor analysis) and the information they provide. All three methods found the same species difficult to classify. However, only correspondence factor analysis could suggest explanations for "misclassifications" as it superimposes the two sets of variables, (sub)species and anatomical variables, thus revealing the correlations between them. The bulbus olfactorius accessorius and the caudal mitral cell layer of the bulbus olfactorius principalis were the most discriminatory **structures** in separating Salamandridae and Plethodontidae. The correspondence factor analysis mapped species very much in line with accepted **taxonomy** and highlighted several current controversies [e.g. positioning of certain newts (T. marmoratus, T. vulgaris, T. alpestris), of Salamandrina terdigitata, and of members of the genus Euproctus]. Mapping of Plethodontidae was less clear-cut than that of Salamandridae with more overlap among genera but was quite consistent with knowledge of brain **structure** complexification. We conclude that relationships derived from analyses of telencephalic **structures** provide valuable information that might help **resolve ambiguities**; we have coined the term "neurotaxonomy" for this approach. Copyright 2002 Elsevier Science Ltd.

L4 ANSWER 4 OF 5 MEDLINE on STN

Full Text

AN 2000121754 MEDLINE

DN PubMed ID: 10658667

TI Phylogenetic relationships of Pleurotus species according to the sequence and secondary **structure** of the mitochondrial small-subunit rRNA V4, V6 and V9 domains.

AU Gonzalez P; Labarere J

CS Laboratory of Molecular Genetics and Breeding of Cultivated Mushrooms, INRA-University Victor Segalen Bordeaux, Villenave d'Ornon, France.. labarere@bordeaux.inra.fr

SO Microbiology (Reading, England), (2000 Jan) Vol. 146 (Pt 1), pp. 209-21. Journal code: 9430468. ISSN: 1350-0872.

CY ENGLAND: United Kingdom

DT Journal; Article; (JOURNAL ARTICLE)

(RESEARCH SUPPORT, NON-U.S. GOV'T)

LA English

FS Priority Journals
OS GENBANK-AF091891; GENBANK-AF091892; GENBANK-AF091893; GENBANK-AF091894;
GENBANK-AF091895; GENBANK-AF091896; GENBANK-AF091897; GENBANK-AF091898;
GENBANK-AF091899; GENBANK-AF091900; GENBANK-AF091901; GENBANK-AF091902;
GENBANK-AF091903; GENBANK-AF091904; GENBANK-AF091905; GENBANK-AF091906;
GENBANK-AF091907; GENBANK-AF091908; GENBANK-AF091909; GENBANK-AF091910;
GENBANK-AF091911; GENBANK-AF091912; GENBANK-AF091913; GENBANK-AF091914;
GENBANK-AF091915; GENBANK-AF091916; GENBANK-AF091917; GENBANK-AF091918;
GENBANK-AF091919; GENBANK-AF091920; +
EM 200003
ED Entered STN: 20 Mar 2000
Last Updated on STN: 20 Mar 2000
Entered Medline: 6 Mar 2000
AB A comparative study of the V4, V6 and V9 domains of the mitochondrial
small-subunit (SSU) rRNA was conducted to evaluate the use of these
sequences to investigate phylogenetic relatedness within the genus
Pleurotus. The PCR products encompassing these regions from 48 isolates
belonging to 16 Pleurotus species were sequenced and compared. From this
comparison, the length and sequence of the three domains were found to be
constant within a species. Significant inter-species variations due to
insertion/deletion events were found, in most cases occurring in regions
not directly involved in the maintenance of the standard SSU rRNA
secondary structure. Phylogenetic analysis based upon these
mitochondrial sequences was in agreement with relationships previously
established by morphological descriptions and with previous studies based
upon the nuclear genome or isozymes; moreover such analysis resolved
some ambiguities in earlier analyses. It was confirmed that P.
ostreatus and P. florida represent a single species, as well as P.
pulmonarius and P. sajor-caju. The phylogenetic analysis also made it
possible to assess the relative positions of P. rattenburyi, P. lampas, P.
sapidus, P. colombinus and P. eryngii. The results clearly showed that
sequences of the V4, V6 and V9 domains of the mitochondrial SSU rRNA could
provide good markers for use in the taxonomy and phylogeny of species of
Basidiomycota. Because of their nucleotide conservation, the major
advantage of these species-specific markers was the possibility to study
only one isolate from each species to determine phylogenetic relatedness.

L4 ANSWER 5 OF 5 MEDLINE on STN
Full Text
AN 1995211273 MEDLINE
DN PubMed ID: 7697190
TI Multiple origins of colonial green flagellates from unicells: evidence
from molecular and organismal characters.
AU Buchheim M A; McAuley M A; Zimmer E A; Theriot E C; Chapman R L
CS Faculty of Biological Science, University of Tulsa, Oklahoma 74104-3189.
SO Molecular phylogenetics and evolution, (1994 Dec) Vol. 3, No. 4, pp.
322-43.
Journal code: 9304400. ISSN: 1055-7903.
CY United States
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 199504
ED Entered STN: 10 May 1995
Last Updated on STN: 10 May 1995
Entered Medline: 28 Apr 1995
AB Phylogenetic hypotheses generated from cladistic analysis of organismal
and molecular data are shown to be generally congruent and/or
complementary for comparisons of unicellular and colonial green algae in
the Chlorophyceae. Cladistic analysis of organismal character data
corroborates the alliance of colonial Stephanosphaera with unicellular
Haematococcus (Haematococcaceae sensu Smith), inferred from previous
studies of nuclear-encoded rRNA sequence data. The organismal data also
support monophyly of the colonial Volvocaceae (sensu Smith). Alliances of
other unicellular taxa, including those ascribed to the "Euchlamydomonas"
Hauptgruppe (sensu Ettl), are not resolved by organismal characters
principally because the structure of the data is skewed to shared
ancestral characters (symplesiomorphies) and unique characters
(autapomorphies) which define individual taxa only. Reanalysis of rRNA

sequence data, with additional sequence data for critical taxa, does not support monophyly of the colonial Volvocaceae (sensu Smith). However, these data are weak in the support of the alternate hypothesis of nonmonophyly. In contrast, relationships among most unicellular flagellates are unambiguously **resolved** by the molecular data. Although the failure of the sequence data to **resolve** relationships among colonial flagellates appears to be due to a sampling of conservative sequences, an ancient, rapid radiation event or **taxon** sampling bias may also be contributing to the **ambiguity** problem. Results from analysis of a combined data set (organismal and molecular) are generally consistent with the inferences of the organismal character data regarding the colonial flagellates and are also consistent with the inferences of the sequence data regarding the unicellular taxa.

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=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS
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SINCE FILE      TOTAL
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FULL ESTIMATED COST
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INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 09:40:10 ON 12 MAR 2009
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68 FILES IN THE FILE LIST IN STINDEX
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search error messages that display as 0* with SET DETAIL OFF.
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1 FILE AQUASCI
28 FILE BIOSIS
5 FILE DISSABS
27 FILES SEARCHED...
1 FILE GENBANK
342 FILE IFIPAT
1 FILE MEDLINE
1 FILE NTIS
1 FILE OCEAN
10 FILE PASCAL
1 FILE PHIN
2356 FILE PROMT
15 FILE RDISCLOSURE
9 FILE SCISEARCH
59 FILES SEARCHED...
30386 FILE USPATFULL
5 FILE USPATOLD
5700 FILE USPAT2
9 FILE WPIDS
9 FILE WPINDEX
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18 FILES HAVE ONE OR MORE ANSWERS, 68 FILES SEARCHED IN STINDEX
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L5 QUE INFORMATION AND ARCHITECTURE AND RESOLV? AND (NAME OR ENTITY)
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F1 30386 USPATFULL
F2 5700 USPAT2
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F4 342 IFIPAT
F5 28 BIOSIS
F6 15 RDISCLOSURE
F7 10 PASCAL
F8 9 SCISEARCH
F9 9 WPIDS
F10 9 WPINDEX
F11 5 DISSABS
F12 5 USPATOLD
F13 1 AQUASCI
F14 1 GENBANK
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F15	1	MEDLINE
F16	1	NTIS
F17	1	OCEAN
F18	1	PHIN

=> file f5-f8 f11 f13-f18
COST IN U.S. DOLLARS

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ENTRY	SESSION
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FULL ESTIMATED COST

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=> s l5; dup rem l6
L6 73 L5

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=> d bib ab 1-65
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-> d bib ab 1-60

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Full Text

AN 2008:675023 BIOSIS

DN PREV200800675022

TI First investigation of the collagen D-band ultrastructure in fossilized vertebrate integument.

AU Lingham-Soliar, Theagarten [Reprint Author]; Wesley-Smith, James

CS Univ KwaZulu Natal, EM Unit, ZA-4000 Durban, South Africa

linghamst@ukzn.ac.za

SO Proceedings of the Royal Society Biological Sciences Series B, (OCT 7 2008) Vol. 275, No. 1648, pp. 2207-2212.

ISSN: 0962-8452.

DT Article

LA English

ED Entered STN: 27 Nov 2008

Last Updated on STN: 27 Nov 2008

AB The ultrastructure of dermal fibres of a 200 Myr thunniform ichthyosaur, Ichthyosaurus, specifically the 67 nm axial repeat D-banding of the fibrils, which characterizes collagen, is presented for the first time by means of scanning electron microscopy (SEM) analysis. The fragment of material investigated is part of previously described fossilized skin comprising an **architecture** of layers of oppositely oriented fibre bundles. The wider implication, as indicated by the extraordinary quality of preservation, is the robustness of the collagen molecule at the ultrastructural level, which presumably contributed to its survival during the initial processes of decomposition prior to mineralization. Investigation of the elemental composition of the sample by SEM-energy dispersive X-ray spectroscopy indicates that calcite and phosphate played important roles in the rapid mineralization and fine replication of the collagen fibres and fibrils. The exceedingly small sample used in the investigation and high level of **information** achieved indicate the potential for minimal damage to prized museum specimens; for example, ultrastructural investigations by SEM may be used to help **resolve** highly contentious questions, for example, 'protofeathers' in the Chinese dinosaurs.

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Full Text

AN 2009:14937 BIOSIS

DN PREV200900014937

TI Anticipatory reward signals in ventral striatal neurons of behaving rats.

AU Khamassi, Mehdi; Mulder, Antonius B.; Tabuchi, Eiichi; Douchamps, Vincent;

Wiener, Sidney I. [Reprint Author]

CS Coll France, CNRS, Lab Physiol Percept and Act, 11 Pl Marcelin Berthelot,

F-75231 Paris 05, France

sidney.wiener@college-de-france.fr

SO European Journal of Neuroscience, (NOV 2008) Vol. 28, No. 9, pp. 1849-1866.

ISSN: 0953-816X.

DT Article

LA English

ED Entered STN: 17 Dec 2008

Last Updated on STN: 17 Dec 2008

AB It has been proposed that the striatum plays a crucial role in learning to select appropriate actions, optimizing rewards according to the principles of 'Actor-Critic' models of trial-and-error learning. The ventral striatum (VS), as Critic, would employ a temporal difference (TD) learning algorithm to predict rewards and drive dopaminergic neurons. This study examined this model's adequacy for VS responses to multiple rewards in rats. The respective arms of a plus-maze provided rewards of varying magnitudes; multiple rewards were provided at 1-s intervals while the rat stood still. Neurons discharged phasically prior to each reward, during both initial approach and immobile waiting, demonstrating that this signal is predictive and not simply motor-related. In different neurons, responses could be greater for early, middle or late droplets in the sequence. Strikingly, this activity often reappeared after the final reward, as if in anticipation of yet another. In contrast, previous TD learning models show decremental reward-prediction profiles during reward consumption due to a temporal-order signal introduced to reproduce accurate timing in dopaminergic reward-prediction error signals. To **resolve** this inconsistency in a biologically plausible manner, we adapted the TD learning model such that input **information** is nonhomogeneously distributed among different neurons. By suppressing reward temporal-order signals and varying richness of spatial and visual input **information**, the model reproduced the experimental data. This validates the feasibility of a TD-learning **architecture** where different groups of neurons participate in solving the task based on varied input **information**.

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AN 2007:311509 BIOSIS

DN PREV200700313995

TI Separate conflict-specific cognitive control mechanisms in the human brain.

AU Egner, Tobias [Reprint Author], Delano, Margaret; Hirsch, Joy

CS Northwestern Univ, Cognit Neurol and Alzheimers Dis Ctr, Feinberg Sch Med, 320 E Super, Searle 11, Chicago, IL 60611 USA
t-egner@northwestern.edu

SO NeuroImage, (APR 1 2007) Vol. 35, No. 2, pp. 940-948.

ISSN: 1053-8119.

DT Article

LA English

ED Entered STN: 16 May 2007

Last Updated on STN: 25 Jul 2007

AB To ensure optimal task performance, the human brain detects and **resolves** conflict in **information** processing via a cognitive control system. However, it is not known whether conflict resolution relies on a single central resource of cognitive control, or on a collection of independent control mechanisms that deal with different types of conflict. In order to address this question, we assessed behavioral and blood-oxygen-level-dependent (BOLD) responses during the simultaneous detection and resolution of two sources of conflict in a modified color-naming Stroop task: conflict stemming from incompatibility between the task-relevant and an irrelevant stimulus feature (stimulus-based or Stroop conflict), and conflict stemming from incompatibility between an irrelevant stimulus feature and response features (response-based or Simon conflict). Results show that control mechanisms recruited by stimulus-based conflict **resolve** stimulus-based conflict, but do not affect the resolution of response-based conflict, and vice versa. The resolution of response-based conflict was distinguished by modulation of activity in premotor cortex, whereas resolution of stimulus-based conflict was distinguished by the modulation of activity in parietal cortex. These results suggest that the human brain flexibly adopts, and independently controls, conflict-specific resolution strategies, biasing motor programming to **resolve** response-based conflict, and biasing stimulus representations to **resolve** stimulus-based conflict. We propose a non-centralized, modular **architecture** of cognitive control, where separate control resources operate in parallel, and are recruited in a context-sensitive manner. (c) 2006 Elsevier Inc. All rights reserved.

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AN 2007:495836 BIOSIS

DN PREV200700497921
 TI Can north american fish passage tools work for South american migratory fishes?.

AU Baigun, Claudio Rafael Mariano [Reprint Author]; Nestler, John Michael; Oldani, Norberto Oscar; Goodwin, R. Andrew; Weber, Larry J.

CS IIB INTECH, Camino Circunvalac Laguna, Km 6, RA-7120 Chascomus, Argentina claudiobaigun@intech.gov.ar; john.m.nestler@erdc.usace.army.mil; rag12@cornell.edu; gbio@ceride.gov.ar; larry-weber@uiowa.edu

SO Neotropical Ichthyology, (APR-JUN 2007) Vol. 5, No. 2, pp. 109-119. ISSN: 1679-6225.

DT Article
 LA English
 ED Entered STN: 20 Sep 2007
 Last Updated on STN: 20 Sep 2007

AB In North America, the Numerical Fish Surrogate (NFS) is used to design fish bypass systems for emigrating juvenile salmon as they migrate from hatchery outfalls and rearing habitats to adult habitat in the oceans. The NFS is constructed of three linked modules: 1) a computational fluid dynamics model describes the complex flow fields upstream of dams at a scale sufficiently resolved to analyze, understand and forecast fish movement, 2) a particle tracking model interpolates hydraulic information from the fixed nodes of the computational fluid model mesh to multiple locations relevant to migrating fish, and 3) a behavior model simulates the cognition and behavior of individual fish in response to the fluid dynamics predicted by the computational fluid dynamics model. These three modules together create a virtual reality where virtual fish exhibit realistic dam approach behaviors and can be counted at dam exits in ways similar to the real world. Once calibrated and validated with measured fish movement and passage data, the NFS can accurately predict fish passage proportions with sufficient precision to allow engineers to select one optimum alternative from among many competing structural or operational bypass alternatives. Although South American fish species are different from North American species, it is likely that the basic computational architecture and numerical methods of the NFS can be used for fish conservation in South America. Consequently, the extensive investment made in the creation of the NFS need not be duplicated in South America. However, its use in South America will require that the behavioral response of the continent's unique fishes to hydrodynamic cues must be described, codified and tested before the NFS can be used to conserve fishes by helping design efficient South American bypass systems. To this end, we identify studies that could be used to describe the movement behavior of South American fishes of sufficient detail that they could be used to develop, calibrate and validate a South American version of the NFS.

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AN 2008:66239 DISSABS Order Number: AAI3310986

TI Integrating business rules of information systems with enterprise architecture

AU Van, Jung Woo [D.Mgt.]; Steenkamp, Annette L. [advisor]

CS Lawrence Technological University (0332)

SO Dissertation Abstracts International, (2006) Vol. 69, No. 5A, p. 1882. Order No.: AAI3310986. 267 pages. ISBN: 978-0-549-60361-0.

DT Dissertation
 FS DAI
 LA English
 ED Entered STN: 20081205
 Last Updated on STN: 20081205

AB < Pub Inc> Due to the inherent complexity of enterprise integration, business rules embedded within the heterogeneous and acquired information systems are often not aligned with the business policies defined in the enterprise strategy. Despite recent research efforts on business rule integration within the scope of enterprise architecture, most research has focused on top-down enterprise strategies of business rule integration, but research on business rule integration of information systems with the enterprise architecture are lacking. This dissertation examines a systematic approach to resolving the business rule integration issues within the enterprise from the perspective of information system business rule integration. In this research

conceptual models for business rule integration are developed. A Business Rule Integration Meta-model Framework (BRIMF), which describes the relationships and associations of the key enterprise **entities** forming the baseline **architecture** for the business rule integration solution, is proposed. A Business Rule Alignment Process Model (BRAPM) and a Business Rule Alignment Methodology (BRAM) are proposed as a formalized approach to align the business rules embedded in **information** systems with the business rules defined in the enterprise **architecture**. A Business Rule Mapping Model (BRMM), which represents one of the stages within the BRAPM, is presented to demonstrate the business rule mapping algorithm as well as identified mapping discrepancy cases. A key benefit of the BRIMF, BRAPM, BRAM and BRMM is the ability to align business rules, extracted from **information** systems, with the business rules defined at the enterprise **architecture** level by using the Business Rule Language Plus (BRL+) for data storage in the enterprise repository. As a constructive validation of the application of the conceptual models a hybrid approach, which adopts mixed techniques to case design and prototyping is employed to demonstrate the effectiveness of the concepts.

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AN 2007:245879 BIOSIS

DN PREV200700250177

TI Advances in Photosynthesis and Respiration:THE LIGHT-DRIVEN PLASTOCYANIN: FERREDOXIN OXIDOREDUCTASE.

AU Golbeck, JH [Editor]

SO Golbeck, JH [Editor]. (2006) Advances in Photosynthesis and Respiration:THE LIGHT-DRIVEN PLASTOCYANIN: FERREDOXIN OXIDOREDUCTASE. Publisher: SPRINGER, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS. Series: ADVANCES IN PHOTOSYNTHESIS AND RESPIRATION. ISBN: 978-1-4020-4255-3(H).

DT Book

LA English

ED Entered STN: 18 Apr 2007

Last Updated on STN: 18 Apr 2007

AB This 716-page book is volume 24 in the series 'Advances in Photosynthesis and Respiration', and this volume summarizes the advances made in the last decade in the biophysics, biochemistry, and molecular biology of the light-driven plastocyanin:ferredoxin oxidoreductase, known as Photosystem I. This reaction center participates with Photosystem II in harvesting solar energy to supply photosynthetic organisms with stored chemical energy in the form of ATP and stored reducing power in the form of NADPH for processes such as metabolism, growth, and reproduction. This volume contains 40 individually-authored chapters divided among 11 thematic parts. Part I of the book focuses on historical perspectives, and part II concentrates on the molecular **architecture** of Photosystem I. Parts III-VIII discuss, respectively, pigment-protein interactions, excitation dynamics and electron transfer processes, modification of the cofactors and their environments, spectroscopic studies of the cofactors, kinetics of electron transfer, and biosynthetic processes. Topics covered in the remaining 3 parts of the book include modeling of photosynthetic processes, related processes, and evolution of Photosystem I. The book is indexed by subject, organism, mutant, and gene and gene product. The book also includes an author index, and a color plate section. The text is written in English. This book is intended to be a comprehensive and up-to-date source of background **information** on Photosystem I for seasoned researchers, those who are just entering the field, Ph.D. students, researchers and advanced undergraduates in the fields of biophysics, biochemistry, microbiology, agriculture, and ecology. Industrial scientists, interested in solar energy conversion, will also find the book useful.

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AN 2007:503835 BIOSIS

DN PREV200700507217

TI Theoretical scenarios for research and development needs to save dwindling sturgeon populations in the Caspian Sea.

AU Mathews, C. P.; Peacock, N.; Gilkolei, R.

CS christophermathews@yahoo.co.uk

SO Journal of Applied Ichthyology, (DEC 2006) Vol. 22, No. Suppl. 1, pp. 132-139.

CODEN: JAICEF. ISSN: 0175-8659.
 DT Article
 General Review; (Literature Review)
 LA English
 ED Entered STN: 26 Sep 2007
 Last Updated on STN: 26 Sep 2007
 AB Current landings of Caspian sturgeon fell from a peak of about 30,000 tonnes in 1977 to about 1,000 tonnes in 2002. Maximum Sustainable Yield (MSY) of Caspian sturgeon is unknown but may be in the range of about 22,500 t/yr. Total Allowable Catches (TACs) fell from about 15,000 t/yr in 1992 to = 500 t/yr in 20022004. It is widely believed that Illegal Unreported and Unregulated (IUU) sturgeon fishing accounts for 90% of real sturgeon landings, but estimates of IUU landings were not included in any TAC assessments. FAO (2004) reported that assessments were not transparent. Rough estimates of stock recovery based on 2002-04 landings and a doubling time of about 14 years suggest that, even in the unlikely event of a total moratorium on legal and (IUU) fishing for about 50 years, stocks could only provide sustainable landings of 4,000 to 8,000 t/yr. Clearly, total recruitment was insufficient to support total effort expended by legal and IUU fishing. In November 1995, after several years of preliminary work and regional consultations, CITES established a ban on international trade in Caspian sturgeon products. Accurate biological data on sturgeon exist in most ex-Soviet countries, but cannot be accessed. Available data on mortality and recruitment do not support dynamic pool, VPA, yield per recruit or stock/recruitment models; catch and effort data are available from Iranian waters from 1990, but can presently not support surplus production modelling of important Caspian wide stocks. It is therefore impossible to apply any of the usual assessment methods to Caspian sturgeon stocks. Nevertheless it is clear that these are depleted, face extinction, and require proactive management starting in the immediate future if they are to be conserved. Accessible data and "guesstimates" have been used in an attempt to identify new scenarios and to inform management. A simple bio-economic model based on available **information** and "guesstimates" about key parameters was used to estimate Recovery Rates (RR, %MSY/year) needed to provide Internal Rates of Return (IRR) of 5%-20%. RRs of around 1.0-2.0% MSY/year are needed to support commercially bankable IRRs of = 10% over 25-50 years. The model suggests that a private sector investment of about = 500,000,000 in restocking, repayable over 50 years, may be feasible. Resulting benefits of such an investment would include from around US 500\$ 1.0 Billion/year for the foreseeable future. Private sector funding will become available only when a transparent and well structured institutional **architecture** is provided for Coastal Zone Management (CZM) of the fishery, so that IUU fishing can be controlled. Issues not addressed by the model that must also be **resolved** include rehabilitation of spawning and nursery grounds, pollution control, careful control of genetic problems associated with restocking, access to sufficient brood stock and full implementation of the Caspian Framework Convention and all of its protocols. Challenges and limitations of such a project are discussed.

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Full Text
 AN 2006:341336 BIOSIS
 DN PREV200600348554
 TI **Resolving** fiber crossing using advanced fast marching tractography based on diffusion tensor imaging.
 AU Staempfli, P.; Jaermann, T.; Crelier, G. R.; Kollias, S.; Valavanis, A.; Boesiger, P. [Reprint Author]
 CS ETH, Inst Biomed Engrn, Gloriastr 35, CH-8092 Zurich, Switzerland
staempfli@biomed.ee.ethz.ch; boesiger@biomed.ee.ethz.ch
 SO NeuroImage, (MAR 2006) Vol. 30, No. 1, pp. 110-120.
 ISSN: 1053-8119.
 DT Article
 LA English
 ED Entered STN: 12 Jul 2006
 Last Updated on STN: 12 Jul 2006
 AB Magnetic resonance diffusion tensor tractography is a powerful tool for the non-invasive depiction of the white matter **architecture** in the human brain. However, due to limitations in the underlying tensor model, the technique is often unable to reconstruct correct trajectories in heterogeneous fiber arrangements, such as axonal crossings. A novel tractography method based on fast marching (FM) is proposed which is

capable of **resolving** fiber crossings and also permits trajectories to branch. It detects heterogeneous fiber arrangements by incorporating **information** from the entire diffusion tensor. The FM speed function is adapted to the local tensor characteristics, allowing in particular to maintain the front evolution direction in crossing situations. In addition, the FM's discretization error is reduced by increasing the number of considered possible front evolution directions. The performance of the technique is demonstrated in artificial data and in the healthy human brain. Comparisons with standard FM tractography and conventional line propagation algorithms show that, in the presence of interfering structures, the proposed method is more accurate in reconstructing trajectories. The in vivo results illustrate that the elucidated major white matter pathways are consistent with known anatomy and that multiple crossings and tract branching are handled correctly. (c) 2005 Elsevier Inc. All rights reserved.

L7 ANSWER 9 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information

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 AN 2006:33037 DISSABS Order Number: AAI3191693
 TI Search and retrieval algorithms for distributed data management systems
 AU Zeinalipour-Yazti, Demetrios [Ph.D.]; Gunopulos, Dimitrios [advisor];
 Kalogeraki, Vana [advisor]
 CS University of California, Riverside (0032)
 SO Dissertation Abstracts International, (2005) Vol. 66, No. 10B, p. 5517.
 Order No.: AAI3191693. 155 pages.
 ISBN: 0-542-34682-6.
 DT Dissertation
 FS DAI
 LA English
 ED Entered STN: 20060621
 Last Updated on STN: 20060621
 AB

Modern Data Management Systems have to cope with data that is generated automatically and continuously across distributed and potentially geographically diverse locations. Organizing **information** in centralized repositories is becoming increasingly expensive and in many occasions impractical.

This dissertation introduces novel search and retrieval algorithms for Distributed Data Management Systems. In our setting, the **information** remains in-situ until users request to retrieve it. Our objective is to minimize the utilization of the communication medium and to exploit the inherent parallelism of a distributed environment. Additionally, I consider the challenges of a graph topology between distributed nodes, which is ubiquitous in emerging fields such as Peer-to-Peer Networks, Sensor Networks and Vehicular Networks.

Specifically, this dissertation makes the following contributions:
 (1) Threshold Join Algorithm (TJA), which is a distributed top-K query processing algorithm that operates over a set of exact scores. TJA uses a non-uniform threshold on the queried attribute in order to minimize the number of data objects that have to be transferred towards the querying node. Additionally, TJA **resolves** queries in the network rather than in a centralized fashion, which minimizes even more the consumption of bandwidth and delay. (2) LB-K and UBLB-K Algorithms, which are specialized distributed top-K query processing algorithms that operate over distributed lower and upper bounds in order to minimize the number of data objects transferred towards the querying engine. (3) Intelligent Search Mechanism (ISM), which is an efficient and scalable technique to route query messages in unstructured Peer-to-Peer systems. ISM is efficient because its performance is bounded by the number of neighbors and scalable because no global knowledge is required to be maintained. ISM also serves as the query routing component in our open source Peerware **architecture**. (4) Distributed Domain Name Order Algorithm (DDNO), which alleviates the burden incurred by the topology mismatch between the underlying physical network and the overlay network of Peer-to-Peer systems, by clustering topologically close-by nodes together.

My dissertation shows that traditional search and retrieval methods can be improved by an order of magnitude by using a combination of local query processing techniques, in-network aggregation and awareness of the underlying network topology.

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STN
AN 2005:309453 BIOSIS
DN PREV200510096386
TI Structural insights into a yeast prion illuminate nucleation and strain diversity.
AU Krishnan, Rajaraman; Lindquist, Susan L. [Reprint Author]
CS Whitehead Inst Biomed Res, 9 Cambridge Ctr, Cambridge, MA 02142 USA
Lindquist_admin@mit.edu
SO Nature (London), (JUN 9 2005) Vol. 435, No. 7043, pp. 765-772.
CODEN: NATUAS. ISSN: 0028-0836.
DT Article
LA English
ED Entered STN: 15 Aug 2005
Last Updated on STN: 26 Sep 2007
AB Self-perpetuating changes in the conformations of amyloidogenic proteins play vital roles in normal biology and disease. Despite intense research, the **architecture** and conformational conversion of amyloids remain poorly understood. Amyloid conformers of Sup35 are the molecular embodiment of the yeast prion known as [PSI], which produces heritable changes in phenotype through self-perpetuating changes in protein folding. Here we determine the nature of Sup35's cooperatively folded amyloid core, and use this **information** to investigate central questions in prion biology. Specific segments of the amyloid core form intermolecular contacts in a 'Head-to-Head', 'Tail-to-Tail' fashion, but the 'Central Core' is sequestered through intramolecular contacts. The Head acquires productive interactions first, and these nucleate assembly. Variations in the length of the amyloid core and the nature of intermolecular interfaces form the structural basis of distinct prion 'strains', which produce variant phenotypes in vivo. These findings **resolve** several problems in yeast prion biology and have broad implications for other amyloids.

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AN 2005-0149318 PASCAL
CP Copyright © 2005 INIST-CNRS. All rights reserved.
TIEN Algorithm for DNSSEC trusted key rollover
IC0IN 2005 : **information** networking : convergence in broadband and mobile networking : Jeju Island, 31 January - 2 February 2005
AU GUETTE Gilles; COUSIN Bernard; FORT David
KIM Cheeha (ed.)
CS IRISA, Campus de Beaulieu, 35042 Rennes, France
SO Lecture notes in computer science, (2005), 3391, 679-688, 14 refs.
Conference: International conference on information networking, (Korea, Republic of), 31 Jan 2005
ISSN: 0302-9743
ISBN: 3-540-24467-0
DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INIST-16343, 354000124442130710
AB The Domain **Name** System Security Extensions (DNSSEC) **architecture** is based on public-key cryptography. A secure DNS zone has one or more keys and signs its resource records with these keys in order to provide two security services: data integrity and authentication. These services allow to protect DNS transactions and permit the detection of attempted attacks on DNS. The DNSSEC validation process is based on the establishment of a chain of trust between zones. This chain needs a secure entry point: a DNS zone whose at least one key is trusted. In this paper we study a critical problem associated to the key rollover in DNSSEC: the trusted keys rollover problem. We propose an algorithm that allows a **resolver** to update its trusted keys automatically and in a secure way without any delay or any break of the DNS service.

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AN 2006-0090448 PASCAL
CP Copyright © 2006 INIST-CNRS. All rights reserved.
TIEN On the controlled evolution of access rules in cooperative **information** systems

On the move to meaningful internet systems 2005 : CoopIS, DOA, and ODBASE
 : OTM Confederated International Conferences, CoopIS, DOA, and ODBASE
 2005, Agia Napa, Cyprus, October 31- November 4, 2005 : proceedings

AU RINDERLE Stefanie; REICHERT Manfred
 CS Department Databases and Information Systems, University of Ulm, Germany,
 Federal Republic of; Information Systems Group, University of Twente,
 Netherlands

SO Lecture notes in computer science, (2005), 3760, 238-255, 29 refs.
 Conference: OTM Confederated International Conferences, Agia Napa
 (Cyprus), 31 Oct 2005
 ISSN: 0302-9743
 ISBN: 3-540-29736-7

DT Journal; Conference
 BL Analytic
 CY Germany, Federal Republic of
 LA English
 AV INIST-16343, 354000138666870140

AB For several reasons enterprises are frequently subject to organizational
 change. Respective adaptations may concern business processes, but also
 other components of an enterprise **architecture**. In particular, changes
 of organizational structures often become necessary. The **information**
 about organizational **entities** and their relationships is maintained in
 organizational models. Therefore the quick and correct adaptation of
 these models is fundamental to adequately cope with changes. However,
 model changes alone are not sufficient to guarantee consistency. Since
 organizational models also provide the basis for defining access rules
 (e.g., actor assignments in workflow management systems or access rules
 in document-centered applications) this **information** has to be adapted
 accordingly (e.g., to avoid non-**resolvable** actor assignments). Current
 approaches do not adequately address this problem, which often leads to
 security gaps and delayed change adaptations. In this paper we present a
 comprehensive approach for the controlled evolution of organizational
 models in cooperative **information** systems. First, we introduce a set of
 operators with well-defined semantics for defining and changing
 organizational models. Second, we present an advanced approach for the
 semi-automated adaptation of access rules when the underlying
 organizational model is changed. This includes a formal part concerning
 both the evolution of organizational models and the adaptation of related
 access rules.

L7 ANSWER 13 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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 STN

AN 2005:383112 BIOSIS
 DN PREV200510159424

TI Does consciousness really collapse the wave function? - A possible
 objective biophysical resolution of the measurement problem.

AU Thaheld, Fred H. [Reprint Author]
 CS 99 Cable Circle 20, Folsom, CA 95630 USA
fthaheld@directcon.net

SO Biosystems, (AUG 2005) Vol. 81, No. 2, pp. 113-124.
 CODEN: BSYMBO. ISSN: 0303-2647.

DT Article
 LA English
 ED Entered STN: 21 Sep 2005
 Last Updated on STN: 21 Sep 2005

AB An analysis has been performed of the theories and postulates advanced by
 von Neumann, London and Bauer, and Wigner, concerning the role that
 consciousness might play in the collapse of the wave function, which has
 become known as the measurement problem. This reveals that an error may
 have been made by them in the area of biology and its interface with
 quantum mechanics when they called for the reduction of any superposition
 states in the brain through the mind or consciousness. Many years later
 Wigner changed his mind to reflect a simpler and more realistic objective
 position which appears to offer a way to **resolve** this issue. The
 argument is therefore made that the wave function of any superposed photon
 state or states is always objectively and stochastically changed within
 the complex **architecture** of the eye in a continuous linear process
 initially for most of the superposed photons, followed by a discontinuous
 nonlinear collapse process later for any remaining superposed photons,
 thereby guaranteeing that only final, measured **information** is presented
 to the brain, mind or consciousness. An experiment to be conducted in the

near future may enable us to simultaneously **resolve** the measurement problem and also determine if the linear nature of quantum mechanics is violated by the perceptual process. (c) 2005 Elsevier Ireland Ltd. All rights reserved.

L7 ANSWER 14 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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STN
AN 2005:380664 BIOSIS
DN PREV200510159031
TI Watching the components of photosynthetic bacterial membranes and their in situ organisation by atomic force microscopy.
AU Scheuring, Simon; Levy, Daniel; Rigaud, Jean-Louis [Reprint Author]
CS CNRS, Inst Curie, UMR 168, 11 Rue Pierre and Marie Curie, F-75231 Paris 05, France
rigaud@curie.fr
SO Biochimica et Biophysica Acta, (JUN 30 2005) Vol. 1712, No. 2, pp. 109-127.
ISSN: 0005-2736.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 21 Sep 2005
Last Updated on STN: 21 Sep 2005
AB The atomic force microscope has developed into a powerful tool in structural biology allowing **information** to be acquired at submolecular resolution on the protruding Structures of membrane proteins. It is now a complementary technique to X-ray crystallography and electron microscopy for structure determination of individual membrane proteins after extraction, purification and reconstitution into lipid bilayers. Moving on from the structures of individual components of biological membranes, atomic force microscopy has recently been demonstrated to be a unique tool to identify in situ the individual components of multi-protein assemblies and to study the supramolecular **architecture** of these components allowing the efficient performance of a complex biological function. Here, recent atomic force microscopy studies of native membranes of different photosynthetic bacteria with different polypeptide contents are reviewed. Technology, advantages, feasibility, restrictions and limits of atomic force microscopy for the acquisition of highly **resolved** images of up to 10 angstrom lateral resolution under native conditions are discussed. From a biological point of view, the new insights contributed by the images are analysed and discussed in the context of the strongly debated organisation of the interconnected network of membrane-associated chlorophyll-protein complexes composing the photosynthetic apparatus in different species of purple bacteria. (c) 2005 Elsevier B.V. All rights reserved.

L7 ANSWER 15 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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STN
AN 2006:207458 BIOSIS
DN PREV200600209186
TI Coherence backscattering spectroscopy (cbs): a novel modality for colorectal cancer (CRC) risk stratification.
AU Roy, Hemant; Kim, Young; Wali, Ramesh; Liu, Yang; Koetsier, Jennifer; Kunte, Dhananjay; Goldberg, Michael J.; Backman, Vadim
SO Gastroenterology, (APR 2005) Vol. 128, No. 4, Suppl. 2, pp. A28.
Meeting Info.: Annual Meeting of the
American-Gastroenterological-Association/Digestive-Disease-Week. Chicago, IL, USA. May 14 -19, 2005. Amer Gastroenterol Assoc.
CODEN: GASTAB. ISSN: 0016-5085.
DT Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 29 Mar 2006
Last Updated on STN: 29 Mar 2006
AB Members of our group have been involved in pioneering light-scattering technologies for diagnosis of dysplasia (Nature 2000, Nature Med 2001). Here we report that a novel depth-**resolved** light scattering technique, CBS, enables detection of the micro-architectural changes of the "field effect" and thus may be utilized for CRC risk-stratification. Coherence backscattering is a phenomenon caused by constructive interference of

light waves traveling timereversed paths and encodes **information** about tissue nano/micro-**architecture**. We have recently overcome the technical obstacles that have prevented previous CBS analysis of (issue, thus providing a means to obtain unparalleled depth-selective ultrastructural **information**. (Optics Letters 2004, Applied Optics 2005). We, therefore, tested the ability of CBS to determine CRC risk.Methods: In order to demonstrate that CBS markers develop early in colon carcinogenesis, we evaluated preneoplastic time-points in the azoxymethane (AOM)-treated rat and MIN mouse models of CRC and compared with age-matched controls. Furthermore, we performed a pilot human trial using 37 patients undergoing screening colonoscopy comparing CBS markers obtained from endoscopically normal mucosa from patients with and without adenomas. CBS analysis was conducted on fresh colonic mucosal biopsies using a CBS apparatus.Results:[GRAPHICS]We analyzed two previously validated spectral markers: spectral slope S.S and the score of first two principal components (PC) obtained from the principal component analysis (Gastroenterology 2004). These parameters were dramatically altered early in neoplasia in models and their relevance in humans was confirmed (see table). Conclusions We demonstrate, for the first time, that CBS analysis of the histologically normal mucosa resulted in unprecedented accuracy in detecting the "field effect". Thus, CBS has considerable promise for tailoring CRC screening strategies based on risk.

L7 ANSWER 16 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
 STN
 AN 2005:154031 BIOSIS
 DN PREV200500153118
 TI Translational neurochemical research in acute human brain injury: The current status and potential future for cerebral microdialysis.
 AU Hillered, Lars [Reprint Author]; Vespa, Paul M.; Hovda, David A.
 CS Dept NeurosciDiv Neurosurg, Univ Uppsala Hosp, SE-75185, Uppsala, Sweden
lars.hillered@neurokir.uu.se
 SO Journal of Neurotrauma, (January 2005) Vol. 22, No. 1, pp. 3-41. print. ISSN: 0897-7151 (ISSN print).
 DT Article
 LA English
 ED Entered STN: 20 Apr 2005
 Last Updated on STN: 20 Apr 2005
 AB Microdialysis (MD) was introduced as an intracerebral sampling method for clinical neurosurgery by Hillered et al. and Meyerson et al. in 1990. Since then MD has been embraced as a research tool to measure the neurochemistry of acute human brain injury and epilepsy. In general investigators have focused their attention to relative chemical changes during neurointensive care, operative procedures, and epileptic seizure activity. This initial excitement surrounding this technology has subsided over the years due to concerns about the amount of tissue sampled and the complicated issues related to quantification. The interpretation of mild to moderate MD fluctuations in general remains an issue relating to dynamic changes of the **architecture** and size of the interstitial space, blood-brain barrier (BBB) function, and analytical imprecision, calling for additional validation studies and new methods to control for in vivo recovery variations. Consequently, the use of this methodology to influence clinical decisions regarding the care of patients has been restricted to a few institutions. Clinical studies have provided ample evidence that intracerebral MD monitoring is useful for the detection of overt adverse neurochemical conditions involving hypoxia/ischemia and seizure activity in subarachnoid hemorrhage (SAH), traumatic brain injury (TBI), thromboembolic stroke, and epilepsy. There is some data strongly suggesting that MD changes precede the onset of secondary neurological deterioration following SAH, hemispheric stroke, and surges of increased ICP in fulminant hepatic failure. These promising investigations have relied on MD-markers for disturbed glucose metabolism (glucose, lactate, and pyruvate) and amino acids. Others have focused on trying to capture other important neurochemical events, such as excitotoxicity, cell membrane degradation, reactive oxygen species (ROS) and nitric oxide (NO) formation, cellular edema, and BBB dysfunction. However, these other applications need additional validation. Although these cerebral events and their corresponding changes in neurochemistry are important, other promising MD applications, as yet less explored, comprise local neurochemical provocations, drug penetration to the human brain, MD as a

tool in clinical drug trials, and for studying the proteomics of acute human brain injury. Nevertheless, MD has provided new important insights into the neurochemistry of acute human brain injury. It remains one of very few methods for neurochemical measurements in the interstitial compartment of the human brain and will continue to be a valuable translational research tool for the future. Therefore, this technology has the potential of becoming an established part of multimodality neuro-ICU monitoring, contributing unique **information** about the acute brain injury process. However, in order to reach this stage, several issues related to quantification and bedside presentation of MD data, implantation strategies, and quality assurance need to be **resolved**. The future success of MD as a diagnostic tool in clinical neurosurgery depends heavily on the choice of biomarkers, their sensitivity, specificity, and predictive value for secondary neurochemical events, and the availability of practical bedside methods for chemical analysis of the individual markers. The purpose of this review was to summarize the results of clinical studies using cerebral MD in neurosurgical patients and to discuss the current status of MD as a potential method for use in clinical decision-making. The approach was to focus on adverse neurochemical conditions in the injured human brain and the MD biomarkers used to study those events. Methodological issues that appeared critical for the future success of MD as a routine intracerebral sampling method were addressed.

L7 ANSWER 17 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
 STN
 AN 2004:462014 BIOSIS
 DN PREV200400464368
 TI AdoMet radical proteins - from structure to evolution - alignment of divergent protein sequences reveals strong secondary structure element conservation.
 AU Nicolet, Yvain; Drennan, Catherine L. [Reprint Author]
 CS Dept Chem 16 573, MIT, 77 Massachusetts Ave, Cambridge, MA, 02139, USA
 cdrennan@mit.edu
 SO Nucleic Acids Research, (2004) Vol. 32, No. 13, pp. 4015-4025. print.
 ISSN: 0305-1048 (ISSN print).
 DT Article
 LA English
 ED Entered STN: 1 Dec 2004
 Last Updated on STN: 1 Dec 2004
 AB Eighteen subclasses of S-adenosyl-L-methionine (AdoMet) radical proteins have been aligned in the first bioinformatics study of the AdoMet radical superfamily to utilize crystallographic **information**. The recently **resolved** X-ray structure of biotin synthase (BioB) was used to guide the multiple sequence alignment, and the recently **resolved** X-ray structure of coproporphyrinogen III oxidase (HemN) was used as the control. Despite the low 9% sequence identity between BioB and HemN, the multiple sequence alignment correctly predicted all but one of the core helices in HemN, and correctly predicted the residues in the enzyme active site. This alignment further suggests that the AdoMet radical proteins may have evolved from half-barrel structures (alphabeta)4 to three-quarter-barrel structures ((06 to full-barrel structures (alphabeta)8. It predicts that anaerobic ribonucleotide reductase (RNR) activase, an ancient enzyme that, it has been suggested, serves as a link between the RNA and DNA worlds, will have a half-barrel structure, whereas the three-quarter barrel, exemplified by HemN, will be the most common **architecture** for AdoMet radical enzymes, and fewer members of the superfamily will join BioB in using a complete (alphabeta)8 TIM-barrel fold to perform radical chemistry. These differences in barrel **architecture** also explain how AdoMet radical enzymes can act on substrates that range in size from 10 atoms to 608 residue proteins.

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 AN 2005-0062200 PASCAL
 CP Copyright © 2005 INIST-CNRS. All rights reserved.
 TIEN The roles of ontology and metadata registry for interoperable databases
 Distributed computing and internet technology : Bhubaneswar, 22-24
 December 2004
 AU LEE Jeong-Oog; KO Myeong-Cheol; PAIK Woojin; HEUNG SEOK JEON; KIM
 Junghwan; KANG Hyun-Kyu; KIM Jinsoo

GHOSH R.K. (ed.); MOHANTY Hrushikesha (ed.)
 CS Dept. of Computer Science, Konkuk University, 322 Danwol-dong,
 Chungju-si, Chungcheongbuk-do, 380-701, Korea, Republic of
 SO Lecture notes in computer science, (2004), 3347, 217-226, 16 refs.
 Conference: 1 IDCIT 2004 ; international conference on distributed
 computing and internet technology, Bhubaneswar (India), 22 Dec 2004
 ISSN: 0302-9743
 ISBN: 3-540-24075-6
 DT Journal; Conference
 BL Analytic
 CY Germany, Federal Republic of
 LA English
 AV INST-16343, 354000124400700220
 AB In order to make multiple autonomous databases to interoperate
 effectively, semantic heterogeneities have to be detected and **resolved**.
 Another difficulty is that users can be allowed to handle **information**
 easily from different heterogeneous databases that refer to the same
 real-world **entity**. To solve these problems, in this paper, I present an
information integration system for interoperable databases using
 metadata registry and ontology. A metadata registry is a place to keep
 facts about characteristics of data that are necessary for data sharing
 and exchange in a specific domain. An ontology defines concepts and
 relations among concepts. The purpose of the proposed **architecture** is
 to define an **information** integration model, which combines
 characteristics of both standard specification of metadata registry and
 functionality of ontology for the concepts and relations.

L7 ANSWER 19 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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 STN
 AN 2005:13183 BIOSIS
 DN PREV200500019073
 TI Solution structure of the Tn3 **resolvase**-crossover site synaptic complex.
 AU Nollmann, Marcelo; He, Jiuya; Byron, Olwyn; Stark, W. Marshall [Reprint
 Author]
 CS Inst Biomed and Life SciDiv Mol Genet, Univ Glasgow, Glasgow, Lanark, G11
 6NU, UK
 SO Molecular Cell, (October 8 2004) Vol. 16, No. 1, pp. 127-137. print.
 ISSN: 1097-2765 (ISSN print).
 DT Article
 LA English
 ED Entered STN: 22 Dec 2004
 Last Updated on STN: 22 Dec 2004
 AB Tn3 **resolvase** is a site-specific DNA recombinase, which catalyzes strand
 exchange in a synaptic complex containing twelve **resolvase** subunits and
 two res sites. Hyperactive mutants of **resolvase** can form a simpler
 complex (X synapse) containing a **resolvase** tetramer and two shorter DNA
 segments at which strand exchange takes place (site 1). We have solved
 the low-resolution solution structure of the purified catalytically
 competent X synapse from small-angle neutron and X-ray scattering data,
 using methods in which the data are fitted with models constructed by
 rigid body transformations of a published crystallographic structure of a
resolvase dimer bound to site I. Our analysis reveals that the two site
 I fragments are on the outside of a **resolvase** tetramer core and provides
 some **information** on the quaternary structure of the tetramer. We
 discuss implications of our structure for the **architecture** of the
 natural synaptic complex and the mechanism of strand exchange.

L7 ANSWER 20 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information
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 AN 2004:46732 DISSABS Order Number: AAI3114885
 TI Discrete-event simulations for control and analysis of distributed systems
 AU Ramakrishnan, Sreeram [Ph.D.]; Wysk, Richard A. [advisor]
 CS The Pennsylvania State University (0176)
 SO Dissertation Abstracts International, (2003) Vol. 64, No. 12B, p. 6271.
 Order No.: AAI3114885. 175 pages.
 DT Dissertation
 FS DAI
 LA English
 ED Entered STN: 20040902

Last Updated on STN: 20040902

AB The concept of simulation-based control has been well-established for discrete-part manufacturing domain. However, issues related to extending that **architecture** to control distributed **entities** have not been **resolved**. As the amount of detail that need to be modeled in a simulation that will be used as a control execution mechanism grows, it necessitates adopting various decomposition methods such as distributed modeling. The main challenge associated with distributed modeling is the synchronization of their clocks and maintaining causality of their interactions. Several simulation-based integration **architectures** that allow for the real time control and/or fast global analysis of distributed systems exist. However, no **architecture** provides a coordination mechanism or an integration framework for distributed simulations that can be used both for real time control and for fast analysis without the need of any rollback mechanisms and allowing the interaction with multipass models that can be used for localized fast analysis.

This thesis primarily focuses on developing a generic, object-oriented modeling methodology and integration framework, Distributed Simulations for Analysis and Control (DISIAC), that enables a set of distributed simulation models, fit within a common **architecture**, to serve as a control execution mechanism and as a tool for global fast analysis. The individual federates have access to multipass models for that **entity** which can serve as a localized fast analysis tool and/or as a decision-making tool. This framework integrates the simulation models with the control execution system, databases with product and production schedule **information**, and simulation models of other **entities** in the distributed system. The **architecture** enables the federation to interact with external optimization tools to respond to any changes in their operating condition.

A Federation Simulation Coordinator (FSC) that coordinates the functioning of the simulation models in both modes is presented along with a variation of exact synchronization mechanism developed in this research. A case study based on a real-life example of a Printed Circuit Board (PCB) assembly supply chain segment is used to illustrate the functioning and the utility of the modeling approach presented in this thesis, and discuss various factors that affect the performance of a system modeled using DISIAC.

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AN 2003:4585 PHIN

DED 12 Feb 2003

TI Faster access to life-saving drugs: how EU legislation might speed up the assessment of drugs that promise significant public health benefits

SO Scrip (2003) No. 2823 Review Issue 2002 p14

DT Newsletter

FS FULL

L7 ANSWER 22 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

Full Text

STN

AN 2004:76224 BIOSIS

DN PREV200400078288

TI Neural mechanisms of cortico-cortical interaction in texture boundary detection: A modeling approach.

AU Thielscher, A. [Reprint Author]; Neumann, H.

CS Department of Psychiatry, University of Ulm, Leimgrubenweg 12-14, 89075, Ulm, Germany

axel.thielscher@medizin.uni-ulm.de

SO Neuroscience, (15 December 2003) Vol. 122, No. 4, pp. 921-939. print. CODEN: NRSCDN. ISSN: 0306-4522.

DT Article

LA English

ED Entered STN: 4 Feb 2004

Last Updated on STN: 4 Feb 2004

AB Texture **information** is an elementary feature utilized by the human visual system to automatically, or preattentively, segment the visual scene. The neural substrate underlying human texture processing as well as the basic computational mechanisms remains largely unknown up to now. We propose a neural model of texture processing which integrates the data obtained by a variety of methods into a common computational framework.

It consists of a hierarchy of bi-directionally linked visual areas each containing topographical maps of mutually interconnected cells. It builds upon the two key hypotheses that (i) texture segmentation is based on boundary detection and that (ii) texture border detection is mainly a function of higher visual cortical areas such as V4. This model, while attempting to explain the processing of textures, is embedded in a more general neural model **architecture** of the infero-temporal pathway of form processing. The model allows to link human performance in texture segmentation with model cell activation patterns, in turn permitting to trace back fundamental psychophysical results on texture processing to their putative neural origins. Most importantly, it enables us to identify and evaluate the functional role of feedback connections between cortical areas in the context of texture processing, namely the suppression of ambiguous cell activities leading to a sharply localized detection of texture boundaries. One of the likely neural origins of modulatory effects on V1 cell activation levels, as observed in electrophysiological studies using single- and multi-unit recordings, can be **resolved**.

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DUPLICATE 3

AN 2004-0207387 PASCAL

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TIEN Design and implementation of the multilingual product retrieval agent through XML and the Semantic networks in EC Service-oriented computing : Trento, 15-18 December 2003

AU MOON Yoo-Jin; KTJOON CHOI; KYONGHO MIN; WAN PYONG KIM; YOUNGHO HWANG; PANKOO KIM; YOUNGSE MUN

ORLOWSKA Maria E. (ed.); WEERAWARANA Sanjiva (ed.); PAPAZOGLU Michael P. (ed.); JIAN YANG (ed.)

CS MIS Department, Hankuk University of Foreign Studies, 270 Imun-dong, Tongdaemun-Gu, Seoul 130-791, Korea, Republic of; School of Computer and Information Sciences, Auckland University of Technology, Auckland 1020, New Zealand; Kunsan University, Kunsan, Cheonbuk 573-701, Korea, Republic of; Chosun University, Kwangju 506-741, Korea, Republic of; Korea National Defense University, Seoul 122-875, Korea, Republic of

SO Lecture notes in computer science, (2003), 2910, 423-433, 21 refs. Conference: 1 ICSOC 2003 : international conference on service-oriented computing, Trento (Italy), 15 Dec 2003
ISSN: 0302-9743
ISBN: 3-540-20681-7

DT Journal; Conference

BL Analytic

CY Germany, Federal Republic of

LA English

AV INIST-16343, 354000117814170290

AB Retrieval for products is an important task for e-commerce, since it represents an interface of the customer contact to e-commerce. And e-commerce should provide customers with easily accessible processes in searching. Especially, the product **information** on the World Wide Web needs integration and standardization to keep the pace of rapid expansion with wide reachable ranges. International standards on product catalogs are converging on UNSPSC (Universal Standard Products and Services Classification). With adoption of this standard, we designed the **architecture** of a multilingual product retrieval agent. The **architecture** is based on the central repository model of product catalog management with a distributed updating process. It also includes the perspectives of buyers and suppliers. In addition, the consistency and version management of product **information** are controlled by UNSPSC. The multilingual product **names** are **resolved** by semantic networks, a thesaurus, and product **name** ontology, which enable the present **architecture** to be expanded to the Semantic Web applications.

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STN

AN 2003:314561 BIOSIS

DN PREV200300314561

TI Phylogeny and evolution of calcareous sponges: Monophyly of Calcinea and Calcarenea, high level of morphological homoplasy, and the primitive nature of axial symmetry.

AU Manuel, Michael [Reprint Author]; Borchhiellini, Carole; Alivon, Eliane; Le Parco, Yannick; Vacelet, Jean; Boury-Esnault, Nicole

CS Centre d'Océanologie de Marseille, Station Marine d'Endoume, UMR-CNRS 6540 DIMAR, Université de la Méditerranée, rue de la Batterie des Lions, 13007, Marseille, France
michael.manuel@univ-jussieu.fr

SO Systematic Biology, (June 2003) Vol. 52, No. 3, pp. 311-333. print.
 ISSN: 1063-5157 (ISSN print).

DT Article
 LA English
 ED Entered STN: 9 Jul 2003
 Last Updated on STN: 9 Jul 2003

AB Because calcareous sponges are triggering renewed interest with respect to basal metazoan evolution, a phylogenetic framework of their internal relationships is needed to clarify the evolutionary history of key morphological characters. Morphological variation was scored at the suprageneric level within Calcispongia, but little phylogenetic information could be retrieved from morphological characters. For the main subdivision of Calcispongia, the analysis of morphological data weakly supports a classification based upon cytological and embryological characters (Calcinea/Calcaronea) rather than the older classification scheme based upon the aquiferous system (Homocoela/Heterocoela). The 18S ribosomal RNA data were then analyzed, both alone and in combination with morphological characters. The monophyly of Calcispongia is highly supported, but the position of this group with respect to other sponge lineages and to eumetazoan taxa is not resolved. The monophyly of both Calcinea and Calcaronea is retrieved, and the data strongly rejected the competing Homocoela/Heterocoela hypothesis. The phylogeny implies that characters of the skeleton **architecture** are highly homoplastic, as are characters of the aquiferous system. However, axial symmetry seems to be primitive for all Calcispongia, a conclusion that has potentially far-reaching implications for hypotheses of early body plan evolution in Metazoa.

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AN 2005:1912 AQUASCI

DN ASFA2 2005

TI An ERP approach for container terminal operating systems

AU Choi, H.R.; Kim, H.S.; Park, B.J.; Park, N.-K.; Lee, S.W.

CS Department of MIS, Dong-A University 840, Hadan-dong, Saha-gu, Busan 604-714, Korea

SO Maritime Policy & Management [Marit. Policy Manage.], (20030900) vol. 30, no. 3, pp. 197-210.
 ISSN: 0308-8839.

DT Journal
 FS ASFA2
 LA English
 SL English

AB The major characteristics of ERP (Enterprise Resource Planning) are an enterprise-wide system that covers all the business functions and information resources, integrated database, built-in best industry practice, packaged software and open **architecture**. ERP enables reduction of system development time, flexibility, standardization of workflow and effective business planning capability. ERP is mainly for the manufacturing industry. However, the principles of ERP can also be applied to container terminal operating systems. This paper presents an ERP system approach for a container terminal. It has clustered the workflow of a container terminal and analysed the business process to generate the best workflows. The integrated database is designed to eliminate redundancy and keep integration. The core of ERP for container terminal is the planning facility such as berth planning and yard planning. The planning capability is very tightly coupled with data flow from client **entities** such as shipping companies. The ERP can handle the existing problems of container terminal operation that are mainly caused by lack of integration of a whole information resource in a container terminal, ad-hoc and poor planning capability, disconnected and incorrect data from client companies. The ERP approach can not only **resolve** the problems of container terminals but also promote adoption of **information** systems for container terminals in the world that have not yet implemented terminal operating systems.

L7 ANSWER 26 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
 STN
 AN 2003:508844 BIOSIS
 DN PREV200300509044
 TI Detection of novel tetracycline resistance gene sequences in soil treated
 with swine manure.
 AU Rodriguez-Minguela, C. M. [Reprint Author]; Tiedje, J. M. [Reprint
 Author]; Jacobs, L. W. [Reprint Author]
 CS Michigan State University, East Lansing, MI, USA
 SO Abstracts of the General Meeting of the American Society for Microbiology,
 (2003) Vol. 103, pp. A-042.
<http://www.asmsusa.org/mtgsrc/generalmeeting.htm>. cd-rom.
 Meeting Info.: 103rd American Society for Microbiology General Meeting.
 Washington, DC, USA. May 18-22, 2003. American Society for Microbiology.
 ISSN: 1060-2011 (ISSN print).
 DT Conference; (Meeting)
 Conference; Abstract; (Meeting Abstract)
 LA English
 ED Entered STN: 29 Oct 2003
 Last Updated on STN: 29 Oct 2003
 AB Understanding the origin and fate of antibiotic resistance requires
 understanding genetic reservoirs that are not only found in the easily
 cultured clinical strains. We used a culture-independent approach to
 detect novel tetracycline resistance genes coding for ribosomal protection
 proteins (RPP) in DNA from manured soils. We chose tetracycline as the
 model since it is widely used in animal agriculture as a growth promoter.
 DNA was extracted from composite soil samples obtained from eight farms
 having different histories of swine manure application as well as from
 nearby control soils that had no manure application. Degenerate primers
 corresponding to a conserved 1.3kb region were used to target nucleotide
 sequences of RPP determinants. These were only detected in samples from a
 field to which pig manure of animals feed with tetracycline as a growth
 promoter was recently applied. Soil samples nearby but from where no
 manure was used yielded no RPP PCR products. Putative RPP genes were
 cloned and selected sequenced. Based on current conventions for the
 classification of RPP's, the analyzed clones were affiliated to other
 previously described determinants. Complete identity to published RPP
 sequences was observed only in three instances. Two clones had potential
 novel genotypes with amino acid sequence identities of 70 and 59% to Tet
 32 and Tet Q, respectively, while a third clone showed 84% amino acid
 sequence identity to Tet W and emerged as a putative new variant of this
 determinant. All partial amino acid sequences contained a GTP-binding
 domain **architecture** very similar to that of previously described RPP's.
 PCR products could readily be detected only in recently manured soils
 suggesting that the resistance gene load is reduced under field
 conditions. This study suggests that potentially novel sequences of RPP
 genes can be recovered from environmental DNA, which would expand extant
 diversity among this gene family, which is largely derived from isolates.
 This **information** and approach should provide a better understanding of
 the ecology of antibiotic resistance genes, and will help **resolve** to
 what degree isolate based studies are lacking.

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 AN 2003-0082642 PASCAL
 CP Copyright © 2003 INIST-CNRS. All rights reserved.
 TIEN Channel islands in a reflective ocean: large scale event distribution in
 heterogeneous networks
 NETWORKING 2002 : networking technologies, services, and protocols ;
 performance of computer and communication networks ; mobile and wireless
 communications : Pisa, 19-24 May 2002
 AU CROWCROFT Jon
 GREGORI Enrico (ed.); CONTI Marco (ed.); CAMPBELL Andrew T. (ed.);
 OMIDYAR Guy (ed.); ZUKERMAN Moshe (ed.)
 CS University of Cambridge, Computer Laboratory, William Gates Building, J J
 Thomson Avenue, Cambridge CB3 0FD, United Kingdom
 SO Lecture notes in computer science, (2002), 2345, 1-9, 41 refs.
 Conference: 2 International IFIP-TC6 networking conference, Pisa (Italy),
 19 May 2002

ISSN: 0302-9743
ISBN: 3-540-43709-6

DT Journal; Conference
BL Analytic
CY Germany, Federal Republic of
LA English
AV INST-16343, 354000108472840010
AB

This is a discussion paper about the possible future use of network and transport level multicast services to support extremely large scale event distribution. To date, event notification services[40] have been limited in their scope due to limitations of the infrastructure. At the same time, Internet network and transport layer multicast services have seen limited deployment due to lack of user demand (with the exception more recently of streaming services, e.g. on Sprint's US core network, and in the Internet II). Recent research in active and reflective middleware suggests a way to **resolve** these two problems at one go. Event-driven and messaging infrastructures are emerging as the most flexible and feasible solution for enabling rapid and dynamic integration of legacy and monolithic software applications into distributed systems. Event infrastructures also support deployment and evolution of traditionally difficult-to-build active systems such as large-scale collaborative environments and mobility aware **architectures**. Event notification is concerned with propagation of state changes in objects in the form of events. A crucial aspect of events is that they occur asynchronously. Event consumers have no control over when events are triggered. On the other hand, event suppliers do not generally know what **entities** might be interested in the events they provide. These two aspects clearly define event notification as a model of asynchronous and de-coupled communication, where **entities** communicate in order to exchange **information**, but do not directly control each other. The IETF is just finishing specifying a family of reliable multicast transport protocols, for most of which there are pilot implementations. Key amongst these for the purposes of this research is the exposure to end systems of router filter functionality in a programmable way, known as Generic Router Assist. This is an inherent part of the Pragmatic General Multicast service, implemented by Reuters, Tibco and Cisco in their products, although it has not been widely known or used outside of the TIBNET products until very recently.

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STN
AN 2003:293720 BIOSIS
DN PREV200300293720
TI IMAGING Ca²⁺ FLUX THROUGH SINGLE N - TYPE VOLTAGE - GATED Ca²⁺ CHANNELS EXPRESSED IN XENOPUS OOCYTES.
AU Demuro, A. [Reprint Author]; Parker, I. [Reprint Author]
CS Neurobiology and Behavior, Univ CA Irvine, Irvine, CA, USA
SO Society for Neuroscience Abstract Viewer and Itinerary Planner, (2002) Vol. 2002, pp. Abstract No. 312.2. <http://sfn.scholarone.com>. cd-rom. Meeting Info.: 32nd Annual Meeting of the Society for Neuroscience. Orlando, Florida, USA. November 02-07, 2002. Society for Neuroscience.
DT Conference; (Meeting)
Conference; (Meeting Poster)
Conference; Abstract; (Meeting Abstract)
LA English
ED Entered STN: 25 Jun 2003
Last Updated on STN: 25 Jun 2003
AB The introduction of patch-clamp recording revolutionized our ability to study the functioning of individual ion channels. Nevertheless, patch-clamp recording suffers from limitations. Channels must be physically accessible to the pipette and seal formation may disrupt local cellular **architecture**; recordings are obtained from only one channel at a time; and it is difficult to change solution in the pipette. We describe the potential of fluorescence microscopy as an advantageous adjunct to study single ion channel activity. Visualization of Ca²⁺ influx through individual N-type Ca²⁺ channels transiently expressed in Xenopus oocytes was carried out using confocal microscopy to image along the scan line in the plane of the membrane. Step depolarizations (20-30 mV) delivered by a two electrode voltage clamp produced local (< 0.6 μm) calcium signals representing stochastic openings of multiple discrete channels along the scan line. Single channel calcium transients (SCCATs)

as brief as 10 ms could be **resolved**, and we were able to determine channel lifetime and latency distributions.)Confocal fluorescence imaging thus provides temporal **information** on channel gating similar to that obtained by patch-clamp recording. Moreover, optical imaging provides spatial **information** from multiple channels, involves minimal disruption and is applicable to channels that are not accessible to a patch pipette. We believe that optical single-channel recording will find many applications for study of the numerous voltage-and ligand-gated channels that have appreciable Ca²⁺ permeability.

L7 ANSWER 29 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text

STN
 AN 2001:489246 BIOSIS
 DN PREV200100489246
 TI Integrated exposure and dose modeling and analysis system. 3. Deposition of inhaled particles in the human respiratory tract.
 AU Lazaridis, Mihalis; Broday, David M.; Hov, Oystein; Georgopoulos, Panos G. [Reprint author]
 CS Rutgers University and UMDNJ, Piscataway, NJ, USA
 SO Environmental Science and Technology, (September 15, 2001) Vol. 35, No. 18, pp. 3727-3734. print.
 CODEN: ESTHAG. ISSN: 0013-936X.

DT Article

LA English

ED Entered STN: 17 Oct 2001

Last Updated on STN: 23 Feb 2002

AB Detailed **information** on the composition-**resolved** size distribution of particulate matter deposited along the human respiratory tract can help linking epidemiological, toxicological, and pathological studies and thus potentially improve the understanding of the origin of pulmonary disorders induced by respirable pathogens. For this purpose, a new mechanistic dosimetry model describing the dynamics of respirable particles in the human airways was developed. Model predictions of transport and fate of inhaled aerosols are based on solutions of the aerosol general dynamic equation, which describes changes in particle size and mass distributions resulting from processes such as nucleation, condensation, coagulation, gas phase chemical reaction, and deposition. To compensate for approximating the three-dimensional problem by considering only axial variations along the airways, boundary layer effects are introduced via appropriate dimensionless transport parameters. The **architecture** of the human lung is described by Weibel's simple regular dichotomous model. An important advantage of the present approach is that it allows testing the significance of intersubject lung morphology and ventilation variability for particle deposition and dose calculations. The model predicts the evolution of size and composition distributions of inhaled particles and the deposition profile along the human lower respiratory tract: in general, model predictions are in qualitative and quantitative agreement with tracheobronchial and alveolar deposition data.

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RESERVED. on STN DUPLICATE 5

AN 2001-0339569 PASCAL

CP Copyright © 2001 INIST-CNRS. All rights reserved.

TIEN The role of satellites in global IT: Trends and implications
 Multimedia Communications over Satellites

AU JAMALIPOUR Abbas; TUNG Tracy
 SALKINTZIS Apostolis K. (ed.)

CS The University of Sydney, United States

SO IEEE personal communications, (2001), 8(3), 5-11, 16 refs.

ISSN: 1070-9916 CODEN: IPCME7

DT Journal

BL Analytic

CY United States

LA English

AV INIST-26674, 354000096496590010

AB Satellite will continue to be an essential element in the establishment of long-distance telecommunications for many years, and it will have a major role in the implementation of the so-called global **information** infrastructure in the future. This is because of the particular feature

of the satellite that can provide wide coverage independent of the actual land distance between any pair of communicating **entities**. The new generation of broadband satellite systems, which can provide high-speed data transmission and connectivity to terrestrial data networks, will create profound changes in all aspects of the emerging data communications applications such as Internet and electronic commerce. In this article we explore characteristics of the future satellite networks and their interoperability with terrestrial wireless and wired networks. The emerging data and IP applications impose new implementation issues on the long-latency and restricted satellite channel that must be **resolved** before such interoperability between satellite and terrestrial networks takes place.

L7 ANSWER 31 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information

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AN 2001:24697 DISSABS Order Number: AAI9984989
TI Establishing the performance impact of persistent, location-independent, identification of resources in distributed systems
AU Stewart, Darin Lewis [Ph.D.]; Williams, James G. [adviser]
CS University of Pittsburgh (0178)
SO Dissertation Abstracts International, (2000) Vol. 61, No. 9B, p. 4830.
Order No.: AAI9984989. 145 pages.
ISBN: 0-599-91879-9.
DT Dissertation
FS DAI
LA English
AB Uniform Resource **Names** (URN), or more generally Persistent, Location-independent Identifiers (PLIs) promise to **resolve** many of the long-standing challenges of resource management in distributed systems. Chief among these problems is the issue of "dead links." Once an **Information Bearing Object** has been registered with a PLI scheme, its availability is, theoretically, assured in perpetuity. The reliability of resource availability implied by this has prompted many system implementers to go to great pains to facilitate inclusion of PLIs, in one form or another, in their **architectures**.

These decisions seem to be based more on faith, enthusiasm, and wishful thinking than on any rational analysis. This is due to the fact that with all of the work and experimentation that has gone into PLIs, the cost of adding persistent identification to a system has yet to be addressed. The availability of such a metric would seem to be essential to making an informed decision on whether and to what extent to adopt such a scheme.

This study examined the retrieval performance of the three currently deployed PLI solutions, the URN-based Object Handle system, Persistent, Uniform Resource Locators (PURL) and System Wide Identifiers for Location Look-up (SWILL). Times were logged for each aspect of the resource resolution location process and analyzed to determine the relative impact of each scheme on retrieval performance in a distributed system. These results were then used to inform the modeling of the resolution process.

This study has shown that contrary to the claims of the producers of PLI resolution schemes there is in fact a dramatic degradation of performance when these systems are integrated into an IT **architecture**. It has been shown that this performance degradation can increase retrieval time by up to a factor of 22, which is clearly not acceptable in a production system.

It has also been shown that there are several discreet factors within both PLI scheme implementation and deployment, which can mitigate this performance degradation. To demonstrate these factors and to provide a means to determine the optimum approach to their development, a queueing network model has been developed and demonstrated.

L7 ANSWER 32 OF 65 NTIS COPYRIGHT 2009 NTIS on STN

AN 2007(13):00135 NTIS Order Number: ADA461095/XAB

TI Generalized Aliasing as a Basis for Program Analysis Tools. Doctoral thesis.

AU O'Callahan, R.
CS Carnegie-Mellon Univ., Pittsburgh, PA. School of Computer Science.
(005343049 423887)

NR ADA461095/XAB; CMU-CS-01-124

295p; Nov 2000

NC Contract(s): F33615-03-1-1330 , F30602-97-2-0031

DT Dissertation
CY United States
LA English
NTE Sponsored in part by the National Science Foundation under Grant No.,
CCR9523972.
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located at 5285 Port Royal Road, Springfield, VA, 22161, USA.
NTIS Prices: PC A14/MF A03
OS GRA&I0713
AB Tools for automatic program analysis promise to improve programmer
productivity by searching and summarizing large bodies of code. However,
the phenomenon of aliasing different **names** being used to refer to the
same data reduces the effectiveness of simple textual analyses. This
dissertation describes the design of a system, Ajax, that addresses this
problem by using semantics-based program analysis as the basis for a
number of different tools to aid Java programmers. To enable the
construction of many tools, Ajax imposes a clean separation between
analysis engines that produce alias **information** and tools that consume
it. Analyses are treated as 'black boxes' satisfying a simple, formal
specification given in terms of the semantics of Java bytecode. Knowing
only this specification, one can build many different tools with only a
small amount of code. The thesis explores the flexibility and efficiency
of the design by describing the construction and evaluation of several
different tools: tools to find dead code, **resolve** Java virtual method
calls, statically check Java downcasts, search for accesses to objects,
and build object models. To support these tools, Ajax includes a novel
static analysis engine for Java called SEMI, based on type inference
with polymorphic recursion. SEMI provides fully context sensitive
analysis of large programs. Using SEMI with the downcast checking tool,
Ajax can prove the safety of more than 50% of the downcast instructions
in some real-life Java programs, such as Sun's bytecode disassembler and
the JavaCC parser generator. Ajax is the first system to address this
particular task. One of the key goals of this thesis is to study issues
bearing on the practical utility of static analysis tools for
programmers. This document describes some of the challenges involved in
building an analysis system for off-the-shelf Java applications, and
suggests some possible avenues for future research.

L7 ANSWER 33 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

Full Text

STN
AN 2001:12422 BIOSIS
DN PREV200100012422
TI Multisite fluorescence in proteins with multiple tryptophan residues.
Apomyoglobin natural variants and site-directed mutants.
AU Tcherkasskaya, Olga [Reprint author]; Bychkova, Valentina E.; Uversky,
Vladimir N.; Gronenborn, Angela M.
CS Laboratory of Experimental and Computational Biology, NCI, National
Institutes of Health, Bethesda, MD, 20892, USA
tcherkasskaya@nih.gov
SO Journal of Biological Chemistry, (November, 2000) Vol. 275, No. 46, pp.
36285-36294. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 27 Dec 2000
Last Updated on STN: 27 Dec 2000
AB Time-**resolved** fluorescence experiments were carried out on a variety of
apomyoglobins with one or two tryptophan (Trp) residues located at
invariant positions 7 and 14 in the primary sequence. In all cases, the
Trp fluorescence kinetics were **resolved** adequately into two discrete
lifetime domains, and decay-associated spectra (DAS) were obtained for
each decay component. The DAS **resolved** for unfolded proteins were
indistinguishable by position of the emission maxima and the spectral
shapes. The folded proteins revealed noticeable differences in the DAS,
which relate to the diverse local environments around the Trp residues in
the individual proteins. Furthermore, the DAS of wild-type protein
possessing two Trp residues were simulated well by that of one Trp mutants
either in the native, molten globule, or unfolded states. Overall,
employing Trp fluorescence and site-directed mutagenesis allowed us to

highlight the conformational changes induced by the single amino acid replacement and generate novel structural **information** on equilibrium folding intermediates. Specifically, it was found that conformational fluctuations in the local cluster around the evolutionarily conserved Trp14 are very similar in the native and molten globule states of apomyoglobins. This result indicates that residues in the E and B helices contributing to this cluster are most likely involved in the stabilization of the overall **architecture** of the structured molten globule intermediate.

L7 ANSWER 34 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
Full Text
 STN
 AN 2000:421012 BIOSIS
 DN PREV200000421012
 TI Vegetative and reproductive innovations of early land plants: Implications for a unified phylogeny.
 AU Renzaglia, Karen Sue [Reprint author]; Duff, R. Joel; Nickrent, Daniel L. [Reprint author]; Garbary, David J.
 CS Department of Plant Biology and Center for Systematic Biology, Southern Illinois University, Carbondale, IL, 62901-6509, USA
 SO Philosophical Transactions of the Royal Society of London B Biological Sciences, (29 June, 2000) Vol. 355, No. 1398, pp. 769-793. print. ISSN: 0962-8436.
 DT Article
 LA English
 ED Entered STN: 4 Oct 2000
 Last Updated on STN: 8 Jan 2002
 AB As the oldest extant lineages of land plants, bryophytes provide a living laboratory in which to evaluate morphological adaptations associated with early land existence. In this paper we examine reproductive and structural innovations in the gametophyte and sporophyte generations of hornworts, liverworts, mosses and basal pteridophytes. Reproductive features relating to spermatogenesis and the **architecture** of motile male gametes are overviewed and evaluated from an evolutionary perspective. Phylogenetic analyses of a data set derived from spermatogenesis and one derived from comprehensive morphogenetic data are compared with a molecular analysis of nuclear and mitochondrial small subunit rDNA sequences. Although relatively small because of a reliance on water for sexual reproduction, gametophytes of bryophytes are the most elaborate of those produced by any land plant. Phenotypic variability in gametophytic habit ranges from leafy to thalloid forms with the greatest diversity exhibited by hepatics. Appendages, including leaves, slime papillae and hairs, predominate in liverworts and mosses, while hornwort gametophytes are strictly thalloid with no organized external structures. Internalization of reproductive and vegetative structures within mucilage-filled spaces is an adaptive strategy exhibited by hornworts. The formative stages of gametangial development are similar in the three bryophyte groups, with the exception that in mosses apical growth is intercalated into early organogenesis, a feature echoed in moss sporophyte ontogeny. A monosporangiate, unbranched sporophyte typifies bryophytes, but developmental and structural innovations suggest the three bryophyte groups diverged prior to elaboration of this generation. Sporophyte morphogenesis in hornworts involves non-synchronized sporogenesis and the continued elongation of the single sporangium, features unique among archegoniates. In hepatics, elongation of the sporophyte seta and archegoniophore is rapid and requires instantaneous wall expandability and hydrostatic support. Unicellular, spiralled elaters and capsule dehiscence through the formation of four regular valves are autapomorphies of liverworts. Sporophytic sophistications in the moss clade include conducting tissue, stomata, an assimilative layer and an elaborate peristome for extended spore dispersal. Characters such as stomata and conducting cells that are shared among sporophytes of mosses, hornworts and pteridophytes are interpreted as parallelisms and not homologies. Our phylogenetic analysis of three different data sets is the most comprehensive to date and points to a single phylogenetic solution for the evolution of basal embryophytes. Hornworts are supported as the earliest divergent embryophyte clade with a moss/liverwort clade sister to tracheophytes. Among pteridophytes, lycophytes are monophyletic and an assemblage containing ferns, Equisetum and psilophytes is sister to seed plants. Congruence between morphological and molecular hypotheses indicates that these data sets are tracking the same phylogenetic signal and reinforces our phylogenetic conclusions. It appears that total

evidence approaches are valuable in **resolving** ancient radiations such as those characterizing the evolution of early embryophytes. More **information** on land plant phylogeny can be found at:
<http://www.science.siu.edu/landplants/index.html>.

L7 ANSWER 35 OF 65 SCISEARCH COPYRIGHT (c) 2009 The Thomson

Full Text

Corporation on STN
AN 2001:545086 SCISEARCH
GA The Genuine Article (R) Number: 449LC
TI Application-layer anycasting: A server selection **architecture** and use in a replicated web service
AU Zegura E W (Reprint)
CS Georgia Inst Technol, Coll Comp, Atlanta, GA 30332 USA (Reprint)
AU Ammar M H; Fei Z; Bhattacharjee S
CS Univ Maryland, Dept Comp Sci, College Pk, MD 20742 USA
CYA USA
SO IEEE-ACM TRANSACTIONS ON NETWORKING, (AUG 2000) Vol. 8, No. 4, pp. 455-466.
ISSN: 1063-6692.
PB IEEE-INST ELECTRICAL ELECTRONICS ENGINEERS INC, 345 E 47TH ST, NEW YORK, NY 10017-2394 USA.
DT Article; Journal
LA English
REC Reference Count: 30
ED Entered STN: 20 Jul 2001
Last Updated on STN: 20 Jul 2001
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Server replication improves the ability of a service to handle a large number of clients. One of the important factors in the efficient utilization of replicated servers is the ability to direct client requests to the "best" server, according to some optimality criteria. In the anycasting communication paradigm, a sender communicates with a receiver chosen from an anycast group of equivalent receivers. As such, anycasting is well suited to the problem of directing clients to replicated servers. This paper examines the definition and support of the anycasting paradigm at the application layer, providing a service that uses an anycast **resolver** to map an anycast domain **name** and a selection criteria into an IP address. By realizing anycasting in the application layer, we achieve flexibility in the optimization criteria and ease the deployment of the service. As a case study, we examine the performance of our system for a key service: replicated web servers. To this end, we develop an approach for estimating the response time that a client will experience when accessing given servers. Such **information** is maintained in the anycast **resolver** that clients query to obtain the identity of the server with the best estimated response time. Our performance collection technique combines server push with **resolver** probes to estimate the expected response time without undue overhead. Our experiments show that selecting a server using our **architecture** and estimation technique can improve the client response time by a factor of two over nearest server selection and by a factor of four over random server selection.

L7 ANSWER 36 OF 65 SCISEARCH COPYRIGHT (c) 2009 The Thomson

Full Text

Corporation on STN
AN 2000:630378 SCISEARCH
GA The Genuine Article (R) Number: 342VE
TI Interaction devices for coordinating cooperative distributed systems
AU Ghenniwa H (Reprint)
CS Univ Western Ontario, Dept Elect & Comp Engr, Cooperat Distributed Syst Engrn Grp, London, ON N6G 1H1, Canada (Reprint)
AU Kamel M
CS Univ Waterloo, Dept Syst Design Engr, Pattern Anal & Machine Intelligence Lab, Waterloo, ON N2L 3G1, Canada
CYA Canada
SO INTELLIGENT AUTOMATION AND SOFT COMPUTING, (2000) Vol. 6, No. 3, pp. 173-184.
ISSN: 1079-8587.
PB AUTOSOFT PRESS, PO BOX 14126, ALBUGUERQUE, NM 87191-4126 USA.
DT Article; Journal
LA English

REC Reference Count: 24
ED Entered STN: 2000
Last Updated on STN: 2000
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A cooperative distributed systems approach is an appropriate design paradigm for many applications, such as manufacturing control and network management. A fundamental problem in this paradigm is how to manage the interdependencies among the **entities**. The solution to this interdependency problem is called coordination. In this paper, coordination has been described in terms of structure and mechanism. This paper focuses on the mechanism aspect of the coordination. It is viewed as a composition of decision points and interaction devices directed to deal with different aspects of the interdependency problem. This paper also provides a coordinated, intelligent rational agent (CIR-Agent) model for cooperative distributed systems. The structure and the **architecture** of the agent are based on its mental state regarding achieving a goal. The agent's structure consists of four main components: problem-solver, pre-interaction, interaction, and execution. There is no global control of coordination allowed in the proposed model, for which the agents utilize different interaction devices to **resolve** their interdependencies.

L7 ANSWER 37 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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STN
AN 1999:135109 BIOSIS
DN PREV199900135109
TI Biochemical characterization and solution structure of nitrous oxide reductase from *Alcaligenes xylosoxidans* (NCIMB 11015).
AU Ferretti, Silvia; Grossmann, J. Guenter; Hasnain, S. Samar; Eady, Robert R.; Smith, Barry E. [Reprint author]
CS Nitrogen Fixation Lab., John Innes Centre, Norwich Res. Park, Colney, Norwich NR4 7UH, UK
SO European Journal of Biochemistry, (Feb., 1999) Vol. 259, No. 3, pp. 651-659. print.
CODEN: EJBCAI. ISSN: 0014-2956.
DT Article
LA English
ED Entered STN: 31 Mar 1999
Last Updated on STN: 31 Mar 1999
AB Nitrous oxide reductase (N2OR) is the terminal enzyme involved in denitrification by microbes. No three-dimensional structural **information** has been published for this enzyme. We have isolated and characterized N2OR from *Alcaligenes xylosoxidans* (AxN2OR) as a homodimer of Mr 134 000 containing seven to eight copper atoms per dimer. Comparison of sequence and compositional data with other N2ORs suggests that AxN2OR is typical and can be expected to have similar domain folding and subunit structure to other members of this family of enzymes. We present synchrotron X-ray-scattering data, analysed using a model-independent method for shape restoration, which gave a approx 20 Å resolution structure of the enzyme in solution, providing a glimpse of the structure of any N2OR and shedding light on the molecular **architecture** of the molecule. The specific activity of AxN2OR was approx 6 µmol of N2O reduced/cntdotmin-1/cntdot (mg of protein)-1; N2OR activity showed both base and temperature activation. The visible spectrum exhibited an absorption maximum at 550 nm with a shoulder at 635 nm. On oxidation with K3Fe(CN)6, the absorption maximum shifted to 540 nm and a new shoulder at 480 nm appeared. Reduction under anaerobic conditions resulted in the formation of an inactive blue form of the enzyme with a broad absorption maximum at 650 nm. As isolated, the enzyme shows an almost featureless EPR spectrum, which changes on oxidation to give an almost completely **resolved** seven-line hyperfine signal in the gII region, g = 2.18, with AII = 40 G, consistent with the enzyme being partially reduced as isolated. Both the optical and EPR spectra of the oxidized enzyme are characteristic of the presence of a CuA centre.

L7 ANSWER 38 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
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STN
AN 1999:304973 BIOSIS
DN PREV199900304973
TI Laser-scanning cytometry: A new instrumentation with many applications.
AU Darzynkiewicz, Zbigniew [Reprint author]; Bedner, Elzbieta; Li, Xun;

CS Gorczyca, Wojciech; Melamed, Myron R.
 Brander Cancer Research Institute, New York Medical College, 19 Bradhurst
 Ave., Hawthorne, NY, 10532, USA
 SO Experimental Cell Research, (May 25, 1999) Vol. 249, No. 1, pp. 1-12.
 print.
 CODEN: ECREAL. ISSN: 0014-4827.
 DT Article
 LA English
 ED Entered STN: 12 Aug 1999
 Last Updated on STN: 12 Aug 1999
 AB The laser-scanning cytometer (LSC) is a microscope-based cytofluorometer
 which has attributes of both flow and image cytometry. Laser-excited
 fluorescence emitted from fluorochromed individual cells on a microscope
 slide is measured at multiple wavelengths rapidly with high sensitivity
 and accuracy. Though the instrument has been available commercially for
 only 3 years, it is already used in a variety of different applications in
 many laboratories. This review focuses on the following unique analytical
 capabilities of LSC which complement those of flow cytometry and
 fluorescence image analysis: (a) the cells are positioned on slides during
 measurement so they may be examined repeatedly over time, a feature useful
 for studies of enzyme kinetics and other time-resolved processes; (b)
 sequential analysis of the same cells can be carried out using different
 immuno- or cytochemical stains or genetic probes, merging information on
 cell immunophenotype, cell functions, expression of particular proteins,
 DNA ploidy and cell cycle position, and/or cytogenetic profile for each
 measured cell; (c) any of the cells measured can be relocated to correlate
 with visual examination by fluorescence or brightfield microscopy or with
 any other parameter; (d) topographic distribution of fluorescence
 measurements within the cell, in cytoplasm vs nucleus, permits analysis of
 the translocation of regulatory molecules such as NFkappaB, p53, etc., and
 is essential for FISH analysis; (e) hyperchromicity of nuclear DNA as
 measured by maximal pixel fluorescence intensity allows one to identify
 cell types differing in degree of chromatin condensation such as mitotic
 or apoptotic cells; (f) analysis of tissue section architecture and of
 the constituents in transected cells within tissue sections by ratiometric
 assays normalized to DNA content extends applications of LSC in clinical
 pathology; (g) because cell loss during sample preparation and staining is
 minimal, samples with a paucity of cells can be analyzed; and (h) analyzed
 cells can be stored indefinitely, e.g., for archival preservation or
 additional analysis. Potential future applications of LSC are discussed.

L7 ANSWER 39 OF 65 MEDLINE on STN
 Full Text
 AN 1999032369 MEDLINE
 DN PubMed ID: 9817431
 TI Leonardo da Vinci: the search for the soul.
 AU Del Maestro R F
 CS Division of Neurosurgery, London Health Sciences Centre, University of
 Western Ontario, Canada.. valerie.denomme@lhsc.on.ca
 SO Journal of neurosurgery, (1998 Nov) Vol. 89, No. 5, pp. 874-87. Ref: 46
 Journal code: 0253357. ISSN: 0022-3085.
 CY United States
 DT Biography
 Historical
 Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Abridged Index Medicus Journals; Priority Journals; History of Medicine
 EM 199812
 ED Entered STN: 15 Jan 1999
 Last Updated on STN: 3 Mar 2000
 Entered Medline: 4 Dec 1998
 AB The human race has always contemplated the question of the anatomical
 location of the soul. During the Renaissance the controversy crystallized
 into those individuals who supported the heart ("cardiocentric soul") and
 others who supported the brain ("cephalocentric soul") as the abode for
 this elusive entity. Leonardo da Vinci (1452-1519) joined a long list
 of other explorers in the "search for the soul." The method he used to
 resolve this anatomical problem involved the accumulation of
 information from ancient and contemporary sources, careful notetaking,
 discussions with acknowledged experts, and his own personal search for the

truth. Leonardo used a myriad of innovative methods acquired from his knowledge of painting, sculpture, and **architecture** to define more clearly the site of the "senso comune"--the soul. In this review the author examines the sources of this ancient question, the knowledge base tapped by Leonardo for his personal search for the soul, and the views of key individuals who followed him.

L7 ANSWER 40 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS

Full Text

RESERVED. on STN
AN 1998-0533676 PASCAL
CP Copyright © 1998 INIST-CNRS. All rights reserved.
TIEN Leonardo da Vinci : the search for the soul
AU DEL MAESTRO R. F.
CS Brain Research Laboratories, Division of Neurosurgery, London Health Sciences Centre, University of Western Ontario, London, Ontario, Canada
SO Journal of neurosurgery, (1998), 89(5), 874-887, 46 refs.
ISSN: 0022-3085 CODEN: JONSAC
DT Journal
BL Analytic
CY United States
LA English
AV INIST-6023, 354000071364770280
AB The human race has always contemplated the question of the anatomical location of the soul. During the Renaissance the controversy crystallized into those individuals who supported the heart ("cardiocentric soul") and others who supported the brain ("cephalocentric soul") as the abode for this elusive **entity**. Leonardo da Vinci (1452-1519) joined a long list of other explorers in the "search for the soul." The method he used to **resolve** this anatomical problem involved the accumulation of **information** from ancient and contemporary sources, careful notetaking, discussions with acknowledged experts, and his own personal search for the truth. Leonardo used a myriad of innovative methods acquired from his knowledge of painting, sculpture, and **architecture** to define more clearly the site of the "senso comune"--the soul. In this review the author examines the sources of this ancient question, the knowledge base tapped by Leonardo for his personal search for the soul, and the views of key individuals who followed him.

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STN
AN 1999:7566 BIOSIS
DN PREV199900007566
TI Pigment-pigment interactions in thylakoids and LHClI of chlorophyll a/c containing alga *Pleurochloris meiringensis*: Analysis of fluorescence-excitation and triplet-minus-singlet spectra.
AU Buechel, C.; Naqvi, K. Razi [Reprint author]; Melo, T. B.
CS Dep. Physics, Norwegian Univ. Science Technology, N-7034 Trondheim, Norway
SO Spectrochimica Acta Part A Molecular and Biomolecular Spectroscopy, (May, 1998) Vol. 54, No. 5, pp. 719-726. print.
ISSN: 1386-1425.
DT Article
LA English
ED Entered STN: 11 Jan 1999
Last Updated on STN: 11 Jan 1999
AB Time-**resolved** triplet-minus-singlet (TmS) difference spectra, DELTAA(lambda; t), fluorescence excitation spectra, X(lambda), and absorption spectra, A(lambda), are used for probing pigment-pigment interactions in the thylakoids (Chla/c-ThyI) and isolated light-harvesting complexes associated with photosystem II (Chla/c-LHCII) of the alga *Pleurochloris meiringensis*, whose chromophores comprise chlorophyll a (Chla), chlorophyll c (Chlc), and several carotenoids. The data provide **information** about interactions between Car*-and-Chla0, Chladag-and-Car0, Cardag-and-Chla0 (where the abbreviation Car stands for carotenoid, an asterisk and a dagger denote singlet and triplet excitation, respectively, and the superscript 0 denotes a molecule in the ground state). In Chla/c-ThyI, the efficiency of Car* foward Chla* transfer (variant phiLT), determined by comparing A(lambda) and X(lambda), is slightly less than unity (ca. 0.85), whereas the efficiency of Chladag foward Cardag transfer of triplet energy (variant phiTT) must be much closer to unity, since no long-lived Chladag could be detected; an interaction between Cardag and

Chla0, already familiar from investigations concerning the TmS spectra of the trimers and aggregates of Chla/b-LHCII (the light-harvesting complex associated with the photosystem II of higher plants), which manifests itself through a depletion signal (in the Qy region of Chla) decaying at the same rate as the Car TmS signal, is observed, and explained likewise. In Chla/c-LHCII, both efficiencies are found to be much lower; the drastic reduction in the two yields is attributed to the perturbation of the native molecular **architecture** of the complex by the detergent used in the isolation procedure. The overall TmS signal from Chla/c-LHCII can be decomposed into two contributions, $\Delta\epsilon_{TA}(\lambda; t) = \Delta\epsilon_{TA1}(\lambda; t) + \Delta\epsilon_{TA2}(\lambda; t)$, where $\Delta\epsilon_{TA1}(\lambda; t)$ with a lifetime of about 8 ps; $\Delta\epsilon_{TA2}(\lambda; t)$, which persists for several hundred microseconds, is contributed by those Chladag molecules which fail to transfer their excitation to a Car neighbour. A comparison of $\Delta\epsilon_{TA1}(\lambda; t)$ with the TmS signal of thylakoids shows differences which parallel those previously reported for the TmS spectra of trimers and aggregates of Chla/b-LHCII: the carotenoid peak at 510 nm is broader, and the Qy depletion signal larger, in the difference spectrum of thylakoids. The absorption spectrum of Chla/c-LHCII show no signs of Chla-Chla excitonic interactions, since the Chla-contribution to the spectrum can be reproduced well by simply red-shifting (by about 200 cm⁻¹) the Q bands and the Soret band in the absorption spectrum of an ethanolic solution of Chla, an observation consistent with the absence, reported in a recent study, of excitonic band in the absorption spectrum of an ethanolic solution of Chla, an observation consistent with the absence, reported in a recent study, of excitonic bands in the circular dichroism spectrum of Chla/c-LHCII.

L7 ANSWER 42 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
[Full Text](#)
 STN
 AN 1998:510105 BIOSIS
 DN PREV199800510105
 TI Lessons learned from an Internet GP **information** system.
 AU Briggs, J. S.; Bradley, M. P.
 CS Object People, Sch. Computer Sci. Math., Univ. Portsmouth, Milton Campus, Locksway Rd., Southsea PO4 8JF, UK
 SO Medical Informatics, (July-Sept., 1998) Vol. 23, No. 3, pp. 245-252.
 print.
 ISSN: 0307-7640.
 DT Article
 LA English
 ED Entered STN: 18 Dec 1998
 Last Updated on STN: 18 Dec 1998
 AB We describe the prototype of an application that in actual use would allow GPs to find out more **information** about consultants at hospitals. This would aid the GP in making the decision about which consultant a patient should be referred to. The requirements of the application from the GP's perspective are described, together with some of the issues that have to be **resolved** before hospitals can provide the necessary **information** in a standard format. The application is implemented as a client-server system using standard Internet technologies such as Java and HTML. This **architecture** has a number of advantages but also revealed some issues concerning security and the format of data, among other things. The project showed that there is a desire for such a system and that desire can be fulfilled at a relatively low cost.

L7 ANSWER 43 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
[Full Text](#)
 STN
 AN 1997:395612 BIOSIS
 DN PREV199799694815
 TI Static and dynamic membrane properties of large-terminal bipolar cells from goldfish retina: Experimental test of a compartment model.
 AU Mennerick, Steven; Zenisek, David; Matthews, Gary [Reprint author]
 CS Dep. Neurobiol. Behavior, SUNY Stony Brook, Stony Brook, NY 11794-5230, USA
 SO Journal of Neurophysiology (Bethesda), (1997) Vol. 78, No. 1, pp. 51-62.
 CODEN: JONEA4. ISSN: 0022-3077.
 DT Article
 LA English
 ED Entered STN: 10 Sep 1997

Last Updated on STN: 10 Sep 1997

AB Capacitance measurements allow direct studies of exocytosis and endocytosis in single synaptic terminals isolated from bipolar neurons of goldfish retina. Extending the technique to intact bipolar cells, with their more complex morphology, requires **information** about the cells' electrotonic **architecture**. To this end, we developed a compartment model of bipolar neurons isolated from goldfish retina and tested the model experimentally. The isolated cells retained morphology similar to that of bipolar neurons in intact goldfish retina. In whole cell recordings, current relaxations in response to 10-mV hyperpolarizing voltage pulses decayed with a biexponential time course. This suggests that the cells may be described by a two-compartment equivalent circuit with compartments corresponding to the soma/dendrites (6-10 pF) and synaptic terminal (2-4 pF), linked by the axial resistance (30-60 M-OMEGA) of the axon. Four lines of evidence validate the equivalent circuit. 1) Similar estimates of somatic/dendritic and terminal capacitance were obtained whether the patch pipette was attached to the soma or to the synaptic terminal. 2) Estimates of the capacitance of the two compartments in intact cells were similar to estimates from somata and terminals that were isolated by cleavage of the connecting axon. 3) When current transients were generated from a more complete computer simulation of a bipolar neuron, analysis of the simulated transients with the use of the simple two-compartment model yielded capacitance estimates similar to those used to set up the simulation. 4) In isolated cells, the model gave estimates of depolarization-evoked increases in capacitance of the synaptic terminal that were quantitatively similar to those measured in terminals that were detached from the rest of the cell. Although in previous studies researchers have attempted to apply a similar equivalent circuit to more geometrically complex cells, morphological correlates of the equivalent-circuit compartments have been elusive. Our results demonstrate that in dissociated bipolar cells, precise morphological correlates can be assigned to the equivalent-circuit compartments. Additionally, the work shows that time-resolved capacitance measurements of synaptic transmitter release are possible in intact, isolated bipolar neurons and may also be feasible in intact tissue.

L7 ANSWER 44 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS

Full Text

RESERVED. on STN
AN 1996-0319440 PASCAL
CP Copyright © 1996 INIST-CNRS. All rights reserved.
TIEN A distributed problem-solving approach to collaborative facility engineering
Computing in civil and structural engineering
AU KHEIRO T.
TOPPING Barry H. V. (ed.); KHAN Asad I. (ed.)
CS Center for Integrated Facility Engineering, Stanford University,
Stanford, CA 94305, United States
Department of Mechanical & Chemical Engineering, Heriot-Watt University,
Edinburgh, United Kingdom
SO Advances in engineering software : (1992), (1996), 25(2-3), 243-252, 20
refs.
ISSN: 0965-9978
DT Journal
BL Analytic
CY United Kingdom
LA English
AV INIST-18222, 354000043657800160
AB A framework for collaborative facility engineering is presented. The framework is based on a distributed problem-solving approach to collaborative facility engineering and employs an integration approach called Agent-Based Software Engineering as an implementation vehicle of this approach. The focal **entity** of this framework is a Multiagent Design Team (MDT) that comprises a collection of software agents (e.g. design software applications with a certain standard communication interface) and a design specialist, which together perform specific design tasks. Multiagent design teams are autonomous and form an organizational structure based on a federation **architecture**. Every multiagent design team surrenders its autonomy to a system program called facilitator, which coordinates the interaction among software agents in the federation **architecture**. Facilitators can be viewed as representatives of one or more teams that facilitate the exchange of

design **information** and knowledge in support of the design tasks they perform. In the federation **architecture**, design specialists collaborate by exchanging design **information** with others via their software agents, and by identifying and **resolving** design conflicts by negotiation. In addition to a discussion of the framework's primary components, its realization in an integrated distributed environment for collaborative building engineering is described.

L7 ANSWER 45 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS

[Full Text](#)

RESERVED. on STN DUPLICATE 8
 AN 1995-0138495 PASCAL
 CP Copyright © 1995 INIST-CNRS. All rights reserved.
 TIEN Group data base design: addressing the view modeling problem
 AU HAYNE S.; SUDHA RAM
 CS Univ. Calgary, MIS, fac. business, Calgary AB, Canada
 SO The Journal of systems and software, (1995), 28(2), 97-116, refs. 1 p.3/4
 ISSN: 0164-1212 CODEN: JSSODM
 DT Journal
 BL Analytic
 CY United States
 LA English
 AV INIST-18071, 354000059410010010
 AB Today's organizations increasingly depend on the use of data base technology to manage their operations. Advances in technology have resulted in increasing the number and complexity of these data bases. Despite their growing complexity, all data bases have one thing in common: each must have gone through either a formal or an 'informal' design process. Data bases must mirror reality accurately, and thus the design process must better capture that reality. The heart of the design process is the conceptual design, data model mapping, and physical design. Our research focuses on providing automated support for the first of these, e.g., conceptual design. Conceptual design is known to be a very difficult and time-consuming phase in the development of data base applications. This article describes the **architecture**, implementation, and use of a distributed graphical group data base design system. The group view modeling system (GVMS) is implemented in Microsoft Windows for networked personal computers. The main purpose of GVMS is to allow multiple designers (or users) to share conceptual design **information** in real time and **resolve** design conflicts through the electronic medium. The underlying data model, semantic data model, is extended to include distribution **information** as well as transactions and is represented as an extended **entity** relationship model. Diagram management techniques are implemented to aid in simplifying large complex designs. A small study demonstrated that groups of data base designers who define their view collectively outperform individuals

L7 ANSWER 46 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

[Full Text](#)

STN
 AN 1994:177171 BIOSIS
 DN PREV199497190171
 TI Effect of genetic **architecture** on the power of human linkage studies to **resolve** the contribution of quantitative trait loci.
 AU Eaves, Lindon J.
 CS Dep. Human Genetics, Va. Commonwealth Univ., P.O. Box 3, Richmond, VA 23298-0003, USA
 SO Heredity, (1994) Vol. 72, No. 2, pp. 175-192.
 CODEN: HDTYAT. ISSN: 0018-067X.
 DT Article
 LA English
 ED Entered STN: 26 Apr 1994
 Last Updated on STN: 26 Apr 1994
 AB The effect of genetic **architecture** (linkage relationships, dominance and two forms of non-allelic interaction) on the power of marker studies to detect, locate and analyse the contributions of specific quantitative trait loci (QTLs) to continuous human traits is considered for randomly mating populations in linkage equilibrium under a two-locus model. The expected regression of the within-sibling-pair mean-square on number of alleles identical by descent (IBD) at two marker loci is explored for every possible pair of markers over a region of the genome containing two QTLs linked loosely (50 CM) or more tightly (20 CM). For the cases

examined, it is shown that epistasis between the pair of QTLs reduces considerably the total amount of **information** available for the location and analysis of the QTL effects. The overall effects of epistasis are more marked when there are duplicate gene interactions (i.e. genes operate in parallel) than when there are complementary interactions (i.e. genes operate in series). However, when there are complementary interactions, the regression approach is almost certain to fail to detect any evidence of epistasis. The numerical analysis suggests that methods of QTL analysis based on IBD in humans are unlikely to offer the **resolving** power that is desirable if QTLs are to be located precisely unless inheritance is very simple or prohibitively large numbers of highly selected individuals are available.

L7 ANSWER 47 OF 65 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on

[Full Text](#)

STN

AN 1993:389389 BIOSIS

DN PREV199396064689

TI Nesting biology and immature stages of the rophitine bees (Halictidae) with notes on the Cleptoparasite Biastes (Anthophoridae) (Hymenoptera: Apoidea).

AU Rozen, Jerome G. Jr.

CS Dep. Entomol., American Museum of Natural History, Central Park West at 79th St., New York, NY 10024, USA

SO American Museum Novitates, (1993) Vol. 0, No. 3066, pp. 1-28.

CODEN: AMUNAL. ISSN: 0003-0082.

DT Article

LA English

ED Entered STN: 23 Aug 1993

Last Updated on STN: 23 Aug 1993

AB **Information** on the nesting biology of the ground nesting Sphecosoma dicksoni (Timberlake) and Conanthalictus conanthi (Cockerell) from the southwestern United States is added to previously published data to provide an understanding of nest **architecture**, cell construction, provisioning, egg deposition, laral feeding behavior, cocoon construction (in the case of S. dicksoni), larval defection, and voltinism of these species. No cleptoparasitic bees are associated with either species at present. Observations on nest provisioning and larval adaptations of the related Palearctic Rophites trispinosus Perez are included. Recovery of an intermediate-stage larva of Biastes emarginatus (Schenck) (Nomadinae: Blastini) from the nest establishes this host association of the cleptoparasite. Its larva and the mature larva of the related genus Neopasites are compared and are found to share many derived features. Based on **information** presented here and on published and unpublished accounts, a synopsis of the biology of the Rophitinae is presented based on 7 genera and 14 species. The synopsis identifies features that seem to be characteristic of the subfamily. The mature larvae of the Rophitinae are characterized on the basis of six genera, and a key to available species is presented. The mature larva of Sphecosoma dicksoni and Conanthalictus conanthi are described taxonomically and compared with larvae of other Rophitinae. Also treated is an immature larva (probably last instar) of Rophites trispinosus. Whereas the mature larvae of S. dicksoni and R. trispinosus share many features with rophitine genera Dufourea and Xeralictus, that of C. conanthi is very different, though clearly sharing significant synapomorphies with the others. Many of its differences appear to be related to the fact that it does not spin a cocoon. The pupa of S. dicksoni is also described, the first such treatment for any member of the subfamily. New **information** on nesting biology and immatures of the rophitines, though supporting the monophyly of the subfamily, does not seem to demonstrate phylogenetic linkages with the Halictinae and Nominae or with the Andrenidae and Melittidae at this time. However, a number of characters are identified and discussed that may eventually be helpful in **resolving** these relationships.

L7 ANSWER 48 OF 65 DISSABS COPYRIGHT (C) 2009 ProQuest Information

[Full Text](#)

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AN 90:21219 DISSABS Order Number: AAR9105906

TI THE APPLICATION OF COMPUTER-SUPPORTED COLLABORATIVE WORK AND KNOWLEDGE-BASED TECHNOLOGY TO THE VIEW MODELING AND INTEGRATION PROBLEMS: A MULTI-USER VIEW INTEGRATION SYSTEM (MUVIS) (DATABASE)

AU HAYNE, STEPHEN CHARLES [PH.D.]; RAM, SUDHA [advisor]

CS THE UNIVERSITY OF ARIZONA (0009)
 SO Dissertation Abstracts International, (1990) Vol. 51, No. 9A, p. 3125.
 Order No.: AAR9105906. 201 pages.
 DT Dissertation
 FS DAI
 LA English
 ED Entered STN: 19921118
 Last Updated on STN: 19921118
 AB This dissertation describes the **architecture**, development and implementation of a network application called MUVIS. MUVIS supports the design of distributed object-oriented databases by groups of potential users. MUVIS is a graphical system implemented on Microsoft Windows for personal computers attached to local area networks. It allows designers to share conceptual design objects in real-time and **resolve** naming conflicts through the electronic medium. It assists these database designers in representing their views and integrating these views into a global conceptual schema. The view integration component is decoupled from the view modeling component. The underlying data model, the Semantic Data Model (SDM), is extended to include distribution **information** and transaction specification. The visual interface to the SDM is an Extended **Entity** Relationship model, yet objects in the SDM are classes (as opposed to **entities** and relationships) and this fact reduces the complexity of the integration. An experiment involving groups of size three and four and individuals modeling a complex case validated the view modeling system. The groups were more efficient and produced higher quality designs than did individuals.

L7 ANSWER 49 OF 65 PASCAL COPYRIGHT 2009 INIST-CNRS. ALL RIGHTS

Full Text

RESERVED. on STN
 AN 1991-0220479 PASCAL
 TIEN Database of research structures in public and private institutions in the south of Italy
 AU BIANCHI G.; BRANDI M. C.; SCARDA A. M.
 CS CNR, ist. studi ric. documentazione sci., Rome 00185, Italy
 SO Journal of information science, (1990), 16(5), 299-310, 10 refs.
 ISSN: 0165-5515 CODEN: JISCDI
 DT Journal
 BL Analytic
 CY Netherlands
 LA English
 AV INIST-14165, 354000015074750040
 AB The methodology of a specific inquiry about the structure and the research activities of the institutions operating in the Mezzogiorno is presented. The project included setting up a conceptual schema which concerns structures, activities and ongoing research projects in public and private institutions. The need to choose a formal data model which will allow the correct execution of the design of the complex conceptual schema has been **resolved** by the adoption of the second generation formal model **Entity** Relationship. The main characteristics of the tool used to develop the database ADEPT (Application Design with **Entity** Relationship Programming Techniques) are explained

L7 ANSWER 50 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 535031 RDISCLOSURE
 TI Distributed system identification
 PA Anonymous
 PI RD 535031 20081110
 PRAI RD 2008-535031 20081023
 SO Research Disclosure, Vol. 535, 11 2008, p. 977
 CODEN: RSDSBB; ISSN: 0374-4353
 LA English
 DT Patent
 GIN 6
 GIS 46836; 51360; 58664; 72344; 53876; 62632

L7 ANSWER 51 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 534003 RDISCLOSURE

TI Routing/forwarding **architecture** for pubsub networking
 PA Anonymous
 PI RD 534003 20081010
 PRAI RD 2008-534003 20080902
 SO Research Disclosure, Vol. 534, 10 2008, p. 829
 CODEN: RSDSBB; ISSN: 0374-4353
 LA English
 DT Patent
 GIN 20
 GIS 57694; 53420; 65352; 60800; 72640; 170904; 126254; 55344; 54096; 61298;
 47090; 61634; 62178; 65700; 58754; 57348; 72872; 59942; 37026; 24120

L7 ANSWER 52 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 511048 RDISCLOSURE
 TI Possible enhancements to code-navigation tools and development
 environments
 PA Anonymous
 PI RD 511048 20061110
 PRAI RD 2006-511048 20061020
 SO Research Disclosure, Vol. 511, 11 2006, p. 1493
 CODEN: RSDSBB; ISSN: 0374-4353
 LA English
 DT Patent
 GIN 8
 GIS 73352; 56586; 550496; 67442; 43516; 38654; 55908; 58086

L7 ANSWER 53 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 487006 RDISCLOSURE
 TI Fault tolerant replication in a constellation of servers
 PA Charles S. Johnson, Ronald M. Cassou, and Shang-Sheng Tung
 PI RD 487006 20041110
 PRAI RD 2004-487006 20041020
 REN XP007134448
 SO Research Disclosure, Vol. 487, 11 2004, p. 1403
 CODEN: RSDSBB; ISSN: 0374-4353
 LA English
 DT Patent
 GIN 21
 GIS 87432; 86792; 89748; 89828; 89772; 91550; 80506; 90184; 87032; 88508;
 90202; 92876; 86148; 87538; 91298; 91784; 86584; 89972; 77470; 31756;
 22058

L7 ANSWER 54 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 466118 RDISCLOSURE
 TI Method for referencing and managing arbitrary font technologies in a
 presentation environment
 PA International Business Machines Corporation
 PI RD 466118 20030210
 PRAI RD 2003-466118 20030120
 REN XP007132282
 SO Research Disclosure, Vol. 466, 02 2003, p. 341
 CODEN: RSDSBB; ISSN: 0374-4353
 LA English
 DT Patent
 GIN 2
 GIS 47016; 21224

L7 ANSWER 55 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
 AN 465205 RDISCLOSURE
 TI Bluetooth hyper-scatternets vis web services
 PA International Business Machines Corporation
 PI RD 465205 20030110
 PRAI RD 2002-465205 20021220
 REN XP007132149

SO Research Disclosure, Vol. 465, 01 2003, p. 188
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 18
GIS 46978; 62168; 40328; 29418; 21182; 14792; 16482; 16364; 15750; 28028;
98936; 41562; 58190; 48970; 44218; 47124; 44876; 9044

L7 ANSWER 56 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 462165 RDISCLOSURE
TI Implementing OpenSSL cryptographic functions using IBM's CCA program
product
PA International Business Machines Corporation
PI RD 462165 20021010
PRAI RD 2002-462165 20020920
REN XP007131462
SO Research Disclosure, Vol. 462, 10 2002, p. 1939
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 2
GIS 49910; 45354

L7 ANSWER 57 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 446190 RDISCLOSURE
TI A generic input and output concept for message flows in MQSeries
integrator V2 supporting physical segregation of organizational units
PA International Business Machines Corporation
PI RD 446190 20010610
PRAI RD 2001-446190 20010520
REN XP007128496
SO Research Disclosure, Vol. 446, 06 2001, p. 1079
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 10
GIS 26508; 53064; 34788; 139244; 41468; 39210; 31290; 18074; 39006; 13746
IPCI G06F
IPCR G06F0009-44 [I,A]; G06F0009-44 [I,C*]
EPC G06F0009-44G2G

L7 ANSWER 58 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 444187 RDISCLOSURE
TI Dynamically structured messaging mechanism
PA International Business Machines Corporation
PI RD 444187 20010410
PRAI RD 2001-444187 20010320
REN XP007128085
SO Research Disclosure, Vol. 444, 04 2001, p. 681
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 11
GIS 52548; 25514; 35386; 26852; 40084; 32022; 37478; 25528; 34478; 78508;
17016

L7 ANSWER 59 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 439140 RDISCLOSURE
TI IBM standard software installer (ISSI)
PA International Business Machines Corporation
PI RD 439140 20001110
PRAI RD 2000-439140 20001020
REN XP001009395; XP007127181
SO Research Disclosure, Vol. 439, 11 2000, p. 2023

CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 8
GIS 37780; 136338; 46484; 49028; 33858; 48516; 42666; 23666
IPCI G06F
IPCR G06F0009-445 [I,A]; G06F0009-445 [I,C*]
EPC G06F0009-445N

L7 ANSWER 60 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 430032 RDISCLOSURE
TI Algorithm for microprocessor frequency identification utility
PA Anonymous
PI RD 430032 20000210
PRAI RD 2000-430032 20000120
REN XP000969015; XP007125494
SO Research Disclosure, Vol. 430, 02 2000, p. 240
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 4
GIS 39080; 58392; 11432; 18168
IPCI G06F
IPCR G06F0011-34 [I,A]; G06F0011-34 [I,C*]
EPC G06F0011-34C

=> d 61-65

L7 ANSWER 61 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 426114 RDISCLOSURE
TI Multi-modal data access
PA International Business Machines Corporation
PI RD 426114 19991010
PRAI RD 1999-426114 19990920
REN XP007124971
SO Research Disclosure, Vol. 426, 10 1999, p. 1393
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 8
GIS 45982; 41440; 53304; 52964; 49944; 52704; 20580; 14494

L7 ANSWER 62 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 423111 RDISCLOSURE
TI Converting HTML to well formed XML with preference based tag expansion
PA International Business Machines Corporation
PI RD 423111 19990710
PRAI RD 1999-423111 19990620
REN XP007124645
SO Research Disclosure, Vol. 423, 07 1999, p. 1011
CODEN: RSDSBB; ISSN: 0374-4353
LA English
DT Patent
GIN 3
GIS 47704; 43654; 43414

L7 ANSWER 63 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.

Full Text

on STN
AN 416150 RDISCLOSURE
TI Routine transaction management in a transaction service
PA International Business Machines Corporation
PI RD 416150 19981210
PRAI RD 1998-416150 19981120
REN XP007123738

SO Research Disclosure, Vol. 416, 12 1998, p. 1720
 CODEN: RSDSBB; ISSN: 0374-4353

LA English
 DT Patent
 GIN 4
 GIS 51038; 28226; 35296; 39582

L7 ANSWER 64 OF 65 RDISCLOSURE COPYRIGHT 2009 KENNETH MASON PUBL.
Full Text
 on STN
 AN 413047 RDISCLOSURE
 TI The user destination model for networkscanning
 PA Anonymous
 PI RD 413047 19980910
 PRAI RD 1998-413047 19980820
 REN XP007123262
 SO Research Disclosure, Vol. 413, 09 1998, p. 1194
 CODEN: RSDSBB; ISSN: 0374-4353

LA English
 DT Patent
 GIN 3
 GIS 45908; 51282; 19018

L7 ANSWER 65 OF 65 GENBANK® COPYRIGHT 2009 on STN

LOCUS (LOC): CP000082 GenBank (R)
 GenBank ACC. NO. (GBN): CP000082 AADI01000000 AADI01000001 AADI01000002
 AADI01000003 AADI01000004 AADI01000005 AADI01000006
 AADI01000007 AADI01000008

GenBank VERSION (VER): CP000082.1 GI:71037566
 CAS REGISTRY NO. (RN): 925303-90-8
 SEQUENCE LENGTH (SQL): 2650701
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 1 Nov 2007
 DEFINITION (DEF): Psychrobacter arcticus 273-4, complete genome.
 SOURCE: Psychrobacter arcticus 273-4
 ORGANISM (ORGN): Psychrobacter arcticus 273-4
 Bacteria; Proteobacteria; Gammaproteobacteria;
 Pseudomonadales; Moraxellaceae; Psychrobacter

COMMENT:
 URL -- <http://www.jgi.doe.gov>
 Contacts: Paul Richardson (microbes@cuba.jgi-psf.org)
 Hector L. Ayala-del-Rio (hlayala@hpcf.upr.edu)
 Finished microbial genomes have been curated to close all gaps with
 greater than 98% coverage of at least two independent clones. Each
 base pair has a minimum q (quality) value of 30 and the total error
 rate is less than one per 50000.

REFERENCE: 1 (bases 1 to 2650701)
 AUTHOR (AU): Ayala-del-Rio,H.L.; Chain,P.; Ponder,M.A.; Di
 Bartolo,G.; Ivanova,N.; Bergholz,P.W.; Hauser,L.;
 Land,M.; Bakermans,C.; Rodrigues,D.; Klappenbach,J.A.;
 Zarka,D.; Larimer,F.; Richardson,P.; Thomashow,M.F.;
 Tiedje,J.M.
 TITLE (TI): Complete sequence of Psychrobacter arcticum 273-4
 JOURNAL (SO): Unpublished

REFERENCE: 2 (bases 1 to 2650701)
 AUTHOR (AU): Copeland,A.; Lucas,S.; Lapidus,A.; Barry,K.; Detter,C.;
 Glavina,T.; Hammon,N.; Israni,S.; Chain,P.; Di
 Bartolo,G.; Ivanova,N.; Hauser,L.; Land,M.; Larimer,F.;
 Pitluck,S.; Richardson,P.
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 JOURNAL (SO): Submitted (23-JUN-2005) US DOE Joint Genome Institute,
 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698,
 USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
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          esterase/lipase/thioesterase
          active site (P550187). RBS
          found."
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          /db-xref="GI:71037588"
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          AQGNHFFVVAHFRSCGIPANGKVIFYNAGDTSEVH
          HMLNLRNENYAHIIYGVGVSLGGNA
          LAKYMGEYDDEALCDGAAVISAFVDMSSAATMH
          SFLSHRIYTPYLLNPIIKKALANE
          ITADEIAAIAKAVKRISDFDNIFTAPRHGYRSKND
          YYHSSALPYLRNVITREPLLLISAK
          DDPFIFGTATPNDVSDSVTILDTAHGGHIGYLRV
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          VSAYFNHIGVPSNKKTK"
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gene      complement(26178..26774
CDS      )
          complement(26178..26774 /locus-tag="Psysc-0023"
          )
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          GRPILNVLQHKSIGNVIIIVRYF
          GGIKLGAGGLTRAYAGSAQAADVEMTLSPYIPMV
          QAQILAEFATEAQCRYIVESLGGS
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          LESSP"
          /locus-tag="Psysc-0024"
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          /EC-number="5.4.99.-"
          /codon-start=1
          /transl-table=11
          /product="ribosomal small subunit
          pseudouridine synthase A"
gene      26978..27697
CDS      26978..27697

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gene      28179..29264
CDS       28179..29264
/translation="MVGNNRMLDKFLSKATELSR
KESKKILHAGEVTVNEQVIKDPGV
HVDIVNDDVQWAGEPLSVATGNRYILLHKPEGFE
CTLKAKEYPIVTDLIAVPELGLSLR
IAGRLDVTITGALLISDDGGWLHRTVSPKHEHAK
VYELTLADAMSDAQANAIKEVAE
GILLEGDHEETKPATLEFIDETHARLTLEQGYH
QVKRMMGYFGNRVVELHRAVSVGH
TLDGLEKGGDSRFLTPEEVVKF"
/locus-tag="Psyc-0025"
/locus-tag="Psyc-0025"
/EC-number="5.3.4.1"
/note="Signal predicted by SignalP
2.0 HMM (Signal peptide probability
1.000) with cleavage site
probability 0.996 at residue 24"
/codon-start=1
/transl-table=11
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protein"
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ACAQPNATDMTNKAVSQKVSQSAQ
TSQNTQAIGTVSKVDSRLRQLLTQAGIKTQITS
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DGKYVVIQGLQKNPSKRVVTKTPARSTSAQIGKP
VSASIKSDILANMGALKNMSAKTP
FFYITAVPGVIWGATLEGVFLLSDDAQYITDGEI
SVIEKGQFTGLDSSFELKNQSVL
TTLDTKQLITYPATSAEKAVIYVATDVNCPYCR
LHKQMSMLNAKGVTVKMGVPIYE
ESPEQMGRGIWCQGNEDSRRLKADKAMLQGMTPA
PATCKTNDVAGNREKAAGLAVMAT
PAIYREDGVLFQASFESEPELEFLGVK"
/locus-tag="Psyc-0026"
gene      complement(29409..30059
)
/note="Signal predicted by SignalP
2.0 HMM (Signal peptide probability
0.935) with cleavage site
probability 0.632 at residue 25"
/locus-tag="Psyc-0026"
CDS       complement(29409..30059
)
/codon-start=1
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/product="hypothetical protein"
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INTQGQANTATKELAAAWAIAASNQVDLKNLIQNL
IIHRGDVNAVVKMQMQIMEKQAD
ELEKQAVQGTSHSDPKPLSYCGINCFTISGQVKY
PLVIEMEREGLIDWKIIDIILP"
/locus-tag="Psyc-0027"
/locus-tag="Psyc-0027"
/function="chaperone activity"
/codon-start=1
/transl-table=11
/product="probable chaperone
protein dnaJ"
/protein-id="AAZ17901.1"
/db-xref="GI:71037593"
/translation="MSKRDFYEILGVSKTADNKE
VKRAYRKLAMKYHPDRNSDDPDAE
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GQSRGGGGGRSRRGSDRLRYIELTLEEAVRGCKK

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EISFTAPAPCDTCDGKGAKNASDI
VTCQTCHGQGVQRMQQGFFAVQQACPHCGGTGKQ
IKNPCSDCHGNGVKDKSRTLEVSI
PAGVDDGDRVRLSGEGAGGAGVQNGDLYVEVRV
KPHNVFTRQGADLYMDVPI SITDA
ALGKEVEIPTLDGKVKIKVAEGTQSGKLLRVGR
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LTREQDLLLRQFDLTLDGDSKHQQSPHKKSFFKK
IGDLFD"
gene      31996..32832    /gene="dapB"
CDS       31996..32832    /locus-tag="Psysc-0028"
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                        /locus-tag="Psysc-0028"
                        /EC-number="1.3.1.26"
                        /function="Diaminopimelate
                        biosynthesis, Lysine biosynthesis
                        via diaminopimellate"
                        /codon-start=1
                        /transl-table=11
                        /product="dihydrrodipicolinate
                        reductase"
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                        /db-xref="GI:71037594"
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                        MVIGTTGFNEQQEQVLAKASEQVAIVYAGNYSTG
                        VNLSLKLLGMAAKAFGTDADVEII
                        EAHKKHKIDAPSGTAYMMAEVAEARGQNLKEVV
                        VYREGQGTGAREAGTIGIHAIRGG
                        EIIGDHTVMFIADGEVVEITHRARARMTFAAGAV
                        RAATWIVQOPVQYQNMQDVLGLND YI"
gene      complement(32915..34090) /locus-tag="Psysc-0029"
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                        /EC-number="4.1.1.17"
                        /function="Putrescine
                        biosynthesis"
                        /codon-start=1
                        /transl-table=11
                        /product="ornithine decarboxylase"
                        /protein-id="AAZ17903.1"
                        /db-xref="GI:71037595"
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                        IYELDRVLDGCGVEASRISYGNTIK
                        KPEHVKYAFDKGIDLYATDSEADLKNIAKHAPGS
                        KIFVRILVQGSSETAEWPLSRKFGC
                        HPNMAIELLIQAQELGLVPYGISFHVGSQQKDVA
                        AWDDALAKVKYMFDMKNNEEGIKL
                        QMINLGGGFPANYLSEVNPVKVYAEIEIKSYLSD
                        YSAEDMPEIILEPGRSLVGSGVL
                        VSDVVLISRSKSHDLTRWVYTDVGLFQGLIETLG
                        EAIKYPVYTPKMETSTSGAGTVVLA
                        GPTCDSTDIMYEEAGYQLPEELEIGDKIFWLTTG
                        AYTNSYSSIEFNGFPFLEVYVYN"
gene      complement(34198..34752) /gene="def"
CDS       complement(34198..34752) /locus-tag="Psysc-0030"
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                        /EC-number="3.5.1.88"
                        /codon-start=1
                        /transl-table=11
                        /product="peptide deformylase"
                        /protein-id="AAZ17904.1"
                        /db-xref="GI:71037596"
                        /translation="MALLPILSYDPRLRMIA

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IGLAASQVDHHIQLIVMDLSEDKDSPRVFINPKV
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ERPKNVRIEAIQNGNAIDEEVEGLLAVCIQHEI
DHLNGVIFVDYLSRLKQTRADKV
RKVLKIREKQGEQVAEKEPQANS"
gene      complement(35124..35378 /locus-tag="Psync-0031"
)
CDS       complement(35124..35378 /locus-tag="Psync-0031"
)
          /note="Signal peptide and 3
          transmembrane helices predicted.
          RBS found."
          /codon-start=1
          /transl-table=11
          /product="conserved hypothetical
          protein"
          /protein-id="AAZ17905.1"
          /db-xref="GI:71037597"
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          MSKRRI"
gene      complement(35713..37230 /gene="mpl"
)
          /locus-tag="Psync-0032"
          /note="Signal predicted by SignalP
          2.0 HMM (Signal peptide probability
          0.973) with cleavage site
          probability 0.475 at residue 25"
CDS       complement(35713..37230 /gene="mpl"
)
          /locus-tag="Psync-0032"
          /codon-start=1
          /transl-table=11
          /product="putative
          UDP-N-acetylmuramate:L-alanyl-gamm
          a-D-glutamyl-meso- diaminopimelate
          ligase"
          /protein-id="AAZ17906.1"
          /db-xref="GI:71037598"
          /translation="MHIHLGICGTFMGSLALLA
          RALGHIVTGSdANIYPPMSTQLEQ
          AGVTIEEGYLIAHLQAPDLVVVGNAMKRGMdVI
          EYMLDTGLRYTSGPQFLSEQVLQS
          RHVIAVAGTHGKTTTTTMLAWILHYAGIDAGFLI
          GGVPLVNTIDTNLQQVFAHSSYLQ
          TEKDDSDNSVNTGYFVIEADEYDSAFFDKRSKFV
          HYRPTAILNNLEFDHADIFADLD
          AIQTQFHHMVRMIPSTGKIIMPAATISLEDTLAK
          GVWPTIWRITSVIDSTISSVRREDS
          PLENSQAENSSDWQAEILISADGSQFTVSFNdNKE
          ATALVNWSMGLHNVNNAIVAAIAA
          AYNIGVSVKTACAALSAFAGIKRRMELIGDVNDI
          LVFDDFAHHPHTAITTTLDGAKKKL
          ADDRLLWAIIEPRSNITMRMGIHQDSLAQSATLADH
          TLWYEPTGLEWGLKEVIDNATIAN
          PSIGSQQVLSSVDDIIKHICTHAKAGDAIVIMSN
          GGFEGIHQRLLTALGNIVAIL"
gene      complement(37523..38146 /locus-tag="Psync-0033"
)
          /note="Signal predicted by SignalP
          2.0 HMM (Signal peptide probability
          0.963) with cleavage site
          probability 0.485 at residue 37"
CDS       complement(37523..38146 /locus-tag="Psync-0033"
)
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="AAZ17907.1"
          /db-xref="GI:71037599"

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/translation="MINFSPVFSTSLIIKRCTSL
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QGAPINSDQSKVLNNDEAVLEENSAKASVNEDR
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SNSDSLQATLMGDYGGVVPSCSGSINITLNLF
ADGSVLKTSVFNQAETPPPLIES
GVYRQDNVDVITIVYEKKNIETYQIQNNHLMIMDE
YKNPDEDYALARQ"
gene      complement(38341..38871) /gene="dsbB"
)
/locus-tag="Psysc-0034"
CDS      complement(38341..38871) /gene="dsbB"
)
/locus-tag="Psysc-0034"
/codon-start=1
/transl-table=11
/product="possible disulfide bond
formation protein"
/protein-id="AAZ17908.1"
/db-xref="GI:71037600"
/translation="MLQLTTYRNQLQVFLVIMTAI
GMSFALFFLQRYMGFSPCPLCIFQ
RIGLMIMGGFALIAALFHPKSMVIRLLLWLGLSLA
GIGWAAIVAGRHVWLQHLPADQVP
SCGPGLDYWLDTLPMQQLVKEVFAGSGECASIEW
TFLGLSIPEQSLILFSILILTHLL
ILWRIVRPSTPKPLAR"
gene      complement(38926..40509) /gene="gshA"
)
/locus-tag="Psysc-0035"
CDS      complement(38926..40509) /gene="gshA"
)
/locus-tag="Psysc-0035"
/EC-number="6.3.2.2"
/function="First step of the
glutathione biosynthesis pathway"
/codon-start=1
/transl-table=11
/product="glutamate-cysteine
ligase"
/protein-id="AAZ17909.1"
/db-xref="GI:71037601"
/translation="MILMSNFASSFVDFDIPNWF
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DELMWPLSMPCMLSNDDEIPLADYSSNTGKLG
TLYRSGLVRYGRRMQTIAGLHYN
LSFGDNLFIAWQAQPTIAQAMLTLEFKNDKYLGL
IRNFKRLTSLVLVLLGASPSVCPC
FVSGIEHDLELFNNSYTYKPTATSLRMGKLGYN
SVQEHLDIRYNNLPEYIKGLRRAI
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SPIRPQIAMSGESPTEALERRGI
AYVEFRAIDLDPYSDIGIRLSACFLEVMAlyCL
LSDSPELMPEEEALAINIERVVN
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LLDAHYGGNDYRAAVALMQGKAGH
SESTISAQVNSDSKRLGSLWQLGFTLAQQHRESL
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AEMEEAETEDFMFLQQYR"
gene      complement(40901..41281) /locus-tag="Psysc-0036"
)
/locus-tag="Psysc-0036"
CDS      complement(40901..41281) /locus-tag="Psysc-0036"
)
/note="Protein of unknown
function, HesB/YadR/YfhF family.
RBS found."
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"

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gene      41787..43805
CDS       41787..43805

/protein-id="AAZ17910.1"
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LNLTDAAQKVRRRLREEEGDSNLM
LRVYVTGGGCSGFSYGFNFANELNEDDANFDNND
VTLVVDLSYQYLQGSTVDYTEGL
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/locus-tag="Psc-0037"
/codon-start=1
/transl-table=11
/product="ABC transporter related
protein, fused ATPase domains"
/protein-id="AAZ17911.1"
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SFQLHPGHVGLTGNNGTGKSLTF
ALLLIRMGITGDTETVLDKGEVSIPDSWHVAHMAQ
EVGATTQTATIDYVLSGDEQWYEIN
ATLNDLSSVSDEQIGVLHQQFDEIDGYRTPTKAA
QIMAGLGFTNQHLEPVEGFSGGW
RMRNLNLAKTLMGRADLMLLDEPTNHLDLDAIWL
ETWINAFTGLVIVISHDQTFDNT
VGHILHVEQQKITLYTGNYYQFIRIRHERMAQQQ
QAFKQEQATKAHLDDFIRRFRAKA
SKAKQASRIKQLERMAELSPMADNPFSSFRFYE
PANMSSPLIELTDADIGYSPTLL
YNANVQVTPDTRIGLLGMNGAGKSTLIKALVGEL
GVLTGSYVSDTLKLYFNQHMD
ILDPKATPIEMLRRLAGKTSAMDLSFLGSFDR
GDRIDITISELFGGGERARILALI
VMQRPNVVLDEPTNHLDLQMRQALITIALQGFEG
AVVLVSHDRELIANVCDEFLVHD
GOIDFDDGDISDYGKWLAEKRKQENSQDKNTSKK
KSKKESKKEVSRRETNANSAGSQAG
KQVGNSESQPALSKDAQKLAEEQRKLTAPIRRD
IETTEKTLATIDEKLLVLEEKLAN
TDLYEESRKADLMTLLNEQTMQLQQQHSQHEEKLL
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/gene="rlpA"

/locus-tag="Psc-0038"
/notes="Signal predicted by SignalP
2.0 HMM (Signal peptide probability
1.000) with cleavage site
probability 0.999 at residue 23"
/gene="rlpA"

CDS       complement(43911..44279)

/locus-tag="Psc-0038"
/function="prc mutant suppressor"
/notes="Lipoprotein conserved
domain"
/codon-start=1
/transl-table=11
/product="putative lipoprotein A"
/protein-id="AAZ17912.1"
/db-xref="GI:71037604"
/translation="MSYLIKSLVITLSILLSATA
FAHNTINTSYGSKFHHGKRTASGSI
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TDRGPFIRGRILDLSKAAAGQINC
QLCTTMEILSYGDGRYRRE"
/locus-tag="Psc-0039"
/locus-tag="Psc-0039"
/function="DnaJ is a chaperone
associated with the Hsp70
heat-shock system involved in
protein folding and renaturation
after stress."
/codon-start=1
/transl-table=11
/product="probable heat shock

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gene          45908..46231
CDS           45908..46231
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              GDGEAYGDGGFRFDDIFSAFGRGARGQTNGQAGG
              QSQYGGFGSQDQSKGQDQHAETVD
              LASVYNGDDYSIKLNVPIRQPNGSVDYDNKTLKI
              KIPKGITDGKQIRLGAQGAAGSGS
              GKNGLDLFKVKLSHAANIRIEGADVQTVNIAPW
              EAALGEKINVSTPAGTILGVTIPKN
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              /codon-start=1
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              protein"
              /protein-id="AAZ17914.1"
              /db-xref="GI:71037606"
              /translation="MKHSPEFNDIIMSDELISA
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              LAEVEQLRLQLKQLDMQAPVIEIN IEHLK"
gene          complement(46320..47522
)
CDS           complement(46320..47522
)
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              /codon-start=1
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              /product="serine/threonine:Na+
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              /protein-id="AAZ17915.1"
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              TELVLVNAVIEVPFANLKEVLINLLMNLVANPV
              NATAEANYIGILAWAIIIGFSLRQ
              ASDTARTVVGDFSDAISQVVKWVIALAPFGILGL
              VANTVAETGFAALAGYARILMVLV
              GCMLFIALVNVNPIILVKTGKNPYPLVFICLRES
              GITAFFTRSSAANIPINMNLARKL
              GLHEDTYSVTIPLGATINMAGAITINVLTLAA
              HTLGIEVTFASALLLSLVATISAC
              GASGVAGGSLLLIPLAASLFSIPNDIAMQVVAIG
              FIIGVIQDSAETALNSSTDVLFETA AADPKYAR"
gene          complement(47861..48319
)
CDS           complement(47861..48319
)
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              /gene="hoIC"
              /locus-tag="Psync-0042"
              /EC-number="2.7.7.7"
              /function="The DNA polymerase III
              holoenzyme is the polymerase
              responsible for the replication of
              the chromosome."
              /note="Chi forms a 1:1 heterodimer
              with psi. The chi:psi complex
              functions by increasing the
              affinity of tau and gamma for
              delta.delta allowing a functional
              clamp-loading complex to form at
              physiological subunit
              concentrations."

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/locus-tag="Psc-0043"
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YKSYQQLGYELTHFNV"
/locus-tag="Psc-0043"
/translation="MNKLTQSLPKHTQKILKK
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SVLQKIANITTYKSTQKRVDSTVAGDITLENQF
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GAAMDEMFKDMGSSAAVLGTIKALCEARLPINVV
GALACAENMPSGDATRPGDIIRAM
NGKSVIELNTDAEGRVLVCDTLCYVQRYQPKAII
DVATLIGACVVALGHVRSVAVFSND
EDVLFDELNASHLSGDLIWHMFMDEYQALDSP
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QYLNKSNAMA"
/locus-tag="Psc-0044"
/translation="MSIPSTLLGLSGGQFNEIDW
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IKMHPNFAFYDTELQALITSAGKQQIIIFAGFMSHM
CVSSSVRAAFDLGFESFVCHDAC
TRDLPVAGQVITASTVHDSAMAALQDRFAALVA
TDKLTNS"
/locus-tag="Psc-0045"
/translation="conserved hypothetical

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gene complement(48355..50013)

CDS complement(48355..50013)

gene complement(50261..50866)

CDS complement(50261..50866)

gene 51384..52634

CDS 51384..52634

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		/db-xref="GI:71037611"
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gene	52634..53842	/locus-tag="Psyc-0046"
CDS	52634..53842	/locus-tag="Psyc-0046"
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		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="AAZ17920.1"
		/db-xref="GI:71037612"
		/translation="MRSLEFEKSPATNHLAAKPTN LKVLSRYVKLNALLAIIAAVIGLW ALQVLFSYLSLSDLSDDSYTMEAKYIFYRSPY FLEQFIPTGALLGAVIGLGLLANN SELVVMRAAGISVYRIVSWVLQPALIFVVLALII NQFVLPHSNQLANEINSGKNSLV TSVRGYWTVPQRFENTKRGITKPDGSDILYIDYA DVKGNIQGVKRWHLDNNGSLQTAI HAEGGQYIGREPLDTVSSKPSQYRYEWQLNMT KLMINQGFESSQAISPTDITLSLFF APESVYLLTHQAEDELSTQLYEHRQFMRQQGQRS LSHELAFWQKLLSLPSILSLVIVA CSFVFGSLRTHSLGLRIVVALLFGLLFSYVQDLV GFVSLATGFSPLLMVLLPIIASAL LGEYLLKRMQ"
gene	complement(53920..54528)	/locus-tag="Psyc-0047"
)	
CDS	complement(53920..54528)	/locus-tag="Psyc-0047"
)	
		/note="Possible 16S RNA G1207 methylase RsmC (COG2813). RBS found."
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="AAZ17921.1"
		/db-xref="GI:71037613"
		/translation="MSHRPPSLLLEKAKYWREDI NFRQDVLGKPFDFATTWGFSPQK LDDGSLMLLDYVDFQNDLSDIDLCGYGVLGMAA ARECPNGQHTLIDKDFMAVEYARL NCEKNGLNNDVDVHLSNGFNHVDKAKDFSLVMSNL PAKVGEQHYLYFLDAHARMKGG RFYVVTINGLRQFMKRSFIEVFGNSEKVKQKTY TITMATKD"
gene	complement(55288..55752)	/locus-tag="Psyc-0048"
)	
		/note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.998) with cleavage site probability 0.955 at residue 22"
CDS	complement(55288..55752)	/locus-tag="Psyc-0048"
)	
		/note="Signal peptide and 5 transmembrane helices predicted."

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protein"
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AVVTALLILFFEPNHTVTLMDVPKQLLGALCGV
PYIVIMVAVQRIQTAVATVAVIF
GQLSMSVLIDNFGLLGNEAISLSGSRISALVCLA
IALFYIYASSNSEPKAQ"
gene      complement(55758..56192
)         /locus-tag="Psync-0049"

/Note="Signal predicted by SignalP
2.0 HMM (Signal peptide probability
0.939) with cleavage site
probability 0.836 at residue 21"
CDS       complement(55758..56192
)         /locus-tag="Psync-0049"

/Note="Signal peptide and 5
transmembrane helices predicted.
RBS found."
/codon-start=1
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protein"
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/db-xref="GI:71037615"
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ALTFFILMLFFSPRDSPPFFSQPPLLVGGLGPV
YVVVLTVTPVIGIALTMIGILAG
QVFQSLIIDHYGLFETMERKIDSKRIALFFIIA
ALFFMAKG"
gene      56291..57226
CDS       56291..57226
/locus-tag="Psync-0050"
/locus-tag="Psync-0050"
/function="The majority of these
proteins appear to be
transcription activators and most
are known to negatively regulate
their own expression. All possess
a potential HTH DNA-binding motif
towards their N-termini."
/codon-start=1
/transl-table=11
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regulator, LysR family"
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APVFFGQRHIAPWLPQLSAQYPKLQIDLSLTDDF
IDPHHYATDVIFRIGTLNDSAFHA
RIFGEQTYHLAASPSYISTHGKLVQPADLTHHCK
LLYKGTGTPNRWLKFTESDWTFF
LAPALLMSNNAESLLVSALKMGIVLFPDWLIGE
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VAAIYPHTRHVS LNVRALIDYFAKVYGHPLYWQL
N"
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/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAZ17925.1"
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IELVSPLYITSSIGGRRQTYKGN

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RHFCEPLVKTEAFTQAAALDIATMVEKLNDEFGQ
DLLMRASVWMTLRESKASFTIEGE
GKELKRIERFAEVMARRTGKGDIPLDPESLAELQ
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TQVNGFKEIVHYIAPPSEDIAKLTGLQALMKKT
EGQSALMRSAVASFAFVYIHPLAD
GNRGVHRFLINDVLRDDQVIEPIILPISQAIIE
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DHYRFDKQAVTYPDGIRSNLNFADSHLIQPAWRF
MDLTPHVQYLSGLIAHVIEKEMHN
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DVFSVVVEIFK"
gene      complement(59255..60193
)          /gene="xerD"
CDS        complement(59255..60193
)          /locus-tag="Psysc-0052"
          /gene="xerD"
          /locus-tag="Psysc-0052"
          /function="Members of this family
          cleave DNA substrates by a series
          of staggered cuts, during which
          the protein becomes covalently
          linked to the DNA through a
          catalytic tyrosine residue at the
          carboxy end of the alignment."
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          integrase"
          /protein-id="AAZ17926.1"
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          KIPTQTARMLSSLRQFYLMWIASN
          LREDNFCERIKSPKLGRLPKDLAEADVNDLLAA
          PDSSTALGLRDKAMLEVLVYACGLR
          VSELVNLSEQVNLNSGWLQITGKGNKTRLVPLG
          EYASDALEDYLTGHRGDLIAHLKA
          GNCQAVFLTAQGGYMTQRNFWYLLKKYAKVASID
          KALSPHTLRHAFATHLLNHGADLR
          SVQLLLGHSNLSTTIQIYTHVATARLQKLHAEHHP
          RG"
gene      complement(60448..61662
)          /locus-tag="Psysc-0053"
CDS        complement(60448..61662
)          /locus-tag="Psysc-0053"
          /note="This protein contains a SAM
          (and some other nucleotide)
          binding motif.  RBS found."
          /codon-start=1
          /transl-table=11
          /product="conserved hypothetical
          protein"
          /protein-id="AAZ17927.1"
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          DEASVTSKVIPNLHFQQRQTQQRSLRLSRLLE
          LDAGYVSQLRRAPDVSACTAFAFG
          ELNESCLLSFRDLQALGAAGVRVKVAIENLGL
          SIFPHYGVFAPTRHEYVQLLLDAP
          LPAYVDVAFDIGTGTGLLAIILAQRGVKQVIATD
          LNPRLACASENLARLELPAVQLQ
          QADLYPTDAPLANLLVCNPPWLPKPTSPLEFAV

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YDANSTMLRGFLQSAKQHLAEHGE
VWLILSDLAEHLQLRSRDELLSWFANAGLEVKYR
LDTPQKHGRSQDDTDPLFAARNAE
ITSLWCLVPFNT"
gene      complement(61869..62129 /locus-tag="Psc-0054"
)
CDS       complement(61869..62129 /locus-tag="Psc-0054"
)
/note="Possible redox protein
regulator of disulfide bond
formation, Sir A. RBS found."
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAZ17928.1"
/db-xref="GI:71037620"
/translation="MTTSTLDSNINHHLDLTQGLI
CPEPVMMLHKIIRKADGGDVIEIL
ATDPATTRDIPNFCRHGLTLVRQEILNDAPTYR
YLVKKSA"
gene      complement(62205..62717 /locus-tag="Psc-0055"
)
CDS       complement(62205..62717 /locus-tag="Psc-0055"
)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
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/translation="MTTVSQSLHNSRRHGFAPL
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TIPLTYNAFIIYRYRLNQTSMVI
MTIGVSSIILIGGLLFADTAWLGLASWLGVAFLF
KVSEKRFNFNLALADLPENNKSAE
NNETITTTDA"
gene      complement(62796..63329 /locus-tag="Psc-0056"
)
CDS       complement(62796..63329 /locus-tag="Psc-0056"
)
/note="This protein contains a
ribonuclease RNase H fold
(COG0816). RBS found."
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAZ17930.1"
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NSLTETARAFDILAMNNGQPDWDNLLGIKVGWV
AKVVVGLPLNMDDGSSSMLSRAHK
FARRLAHRIMEQHLFPVIVSLCDERLTSVAAREIA
WENGWIQNERDPIDDISACILMST
YFADPNSSIAIDAIKAD"
gene      complement(63380..63943 /gene="algH"
)
CDS       complement(63380..63943 /gene="algH"
)
/locus-tag="Psc-0057"
/note="contains putative DNA
binding region also has domain hit
to protein DUF 179"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="AAZ17931.1"
/db-xref="GI:71037623"

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/translation="MSKANLTHHFLIAAPELSDP
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YPEVGFVLHTGQPEWASSFAISEN
VCITTSQDILKRIAAGQGVGHYQLCLGHASWGKK
QLDQELANGDWLVCPADLNLFFDT
PFERWQIAADKIGVNFYDLSSDIGHA"
gene      complement(64062..65741
)          /gene="recN"
CDS        complement(64062..65741
)          /locus-tag="Psysc-0058"
           /gene="recN"
           /locus-tag="Psysc-0058"
           /function="All proteins in this
           family (TIGR00634) for which
           functions are known are ATP
           binding proteins involved in the
           initiation of recombination and
           recombinational repair."
           /codon-start=1
           /transl-table=11
           /product="possible DNA repair
           protein"
           /protein-id="AAZ17932.1"
           /db-xref="GI:71037624"
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AEGFNVIETGETGAGKSLLLDALSL
CVGERADMANVRHGAHAHADIYAQFDVENNPVIAE
WFAKNERALEEPEVLIRRLNNTG
RSKAWLNGTPVSLAELKSLGSLLVNIHSQHAQQA
LLKQPQFVQWLDMAQITSLTTKT
TSSYQYQQLKRRADDLASREAQRDRIQLLQSQ
LADIAPLLVVDYAEVEAEHEELSN
IEALMIEASHGLHLLDNDTDEPDVMTLLGQAIKL
CDNQMSVSQTFEQASEQLHLAQOQ
ITEVTSLLSDYAEQQLPDPERLQSLDSLISLGH
LSRKHNLPANDLINEAKGWAEQLE
QLENEPSSDAMAVQIEQAWQEIYALATELNKERS
KAAPIVSKQLIKOLQPLALPNARC
EFVETIKKTQVSYNGQGCYDIDLFSANVGMPMQ
FLHKIASGGELSRMALVMQVLQAT
NADNNAAKPMLVFEVDVVGISGGTAQVVGELLRA
LGQTQQLLAITHQAQVAAQAHQHI
LVQKHHDEQTESLVLTESDQVDELARMSGGVI
ITDVTDRHARSLLSDVK"
gene      66427..66762
CDS        66427..66762
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           /protein-id="AAZ17933.1"
           /db-xref="GI:71037625"
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DNLVEHYHFSINTSERIEITIGGECEVKINGEAAF
SYYRAGQSFVVEGNSGFNLRTIEI
VQYICHLEG"
gene      66968..67738
CDS        66968..67738
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           /codon-start=1
           /transl-table=11
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           methyltransferase, TrmH family,
           group 3"
           /protein-id="AAZ17934.1"
           /db-xref="GI:71037626"
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PLDGLSLFVQQGRETDSHVQAIMA
QARDNGISIQPTQDKLTLQCSPQHGVVNLNAR
PLGFADEGLLDTLAGREDCLLLVL
DQITDAHNFGACLRITAVAMGVDAVCPKHHAASL

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TPTVAKVSVGAEMMPIVSVTNLA
RTLTKIKNAGVFVFGTALNADAKPLHTADLTGKI
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IPMSGNEHGNLQSLNVSVATGMALYEINRQRTLA
AGQA"
gene      complement(67701..68393) /gene="coaE"
)
/locus-tag="Psysc-0061"
CDS      complement(67701..68393) /gene="coaE"
)
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/EC-number="2.7.1.24"
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WVLNINGDMDRAAVRTHVFTYDPA
LIELEAITHPAIREAAKLQLAESTSPYVLSAPL
LIEAAEAGLANLCQRIIVMDATED
TQLARASQRDALSVQIKAIMVNLQSLREERNLHA
DDVVLNENDLAALYAQLEPLHQDY
LKLAQQLKFAAD"
gene      complement(68477..69376) /gene="pilD"
)
/locus-tag="Psysc-0062"
CDS      complement(68477..69376) /gene="pilD"
)
/locus-tag="Psysc-0062"
/EC-number="3.4.23.43"
/function="cysteine-type peptidase
activity"
/codon-start=1
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/product="type 4 prepilin
peptidase 1. Aspartic peptidase.
MEROPS family A24A"
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WIVLRGRCSSECKTTIGRLYPVVELVTALLSVLVI
YQFVSTAGLSALILVWTLVVLTG
IDFDITQLLPDRLTFFLAGLGLAVNSQGWVFSPTQ
SIWGLLLGLFSLWIVWIKFYLTIK
KHGMGGQDFKLLAVLGAWLGPVMLPLVILLSSLL
GSIVGLLILIKKQGESKPFAGPYI
AIAGIVALLYGSDIVNWWYLGMYN"
gene      complement(69402..70625) /gene="pilC"
)
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CDS      complement(69402..70625) /gene="pilC"
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assembly system protein, PilC"
/protein-id="AAZ17937.1"
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GQVKGETTSHSLELAKATILRKQG
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KDLVLQIKADIEAGGNFASALRRHPRYFDDLFCFS

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LVDSGEQSGALETMLERVATYKEK
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FLDRVALKAP1FGNIYQAVIARF
ARTLSTTTAAGVPLIDALDSTAGANNVVFYNAI
QQIKNDVSTGQQLQFS1IRSTNLF
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gene      complement(70862..72637 /gene="pilB"
)
CDS       complement(70862..72637 /locus-tag="Psysc-0064"
)         /gene="pilB"
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assembly system protein, PilB"
          /protein-id="AAZ17938.1"
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DLVDEKIVRKFNALPMFKRGORLFVALSDPTRID
AIDAIAFNRLSIETVTVVEEDKLE
RCIENLYADTMQSFDSFSDSDNLIGFDESEEDS
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GSTNISTAEDPVEINLEGINQVNV
NPKVGLTFSTALKSFLRQDDPDIVMVGEIRDLETA
EIAIKAAQTGHMVLSTLHTNSAPE
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TDNIIYEPVGCNKCREGYKGRVGIYEVMKITPDI
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LRRSGVLKVLQGVTSIQEMMRVTSG"
gene      73127..73936 /gene="tpiA"
CDS       73127..73936 /locus-tag="Psysc-0065"
          /gene="tpiA"
          /locus-tag="Psysc-0065"
          /EC-number="5.3.1.1"
          /function="catalyzes the
reversible interconversion of
glyceraldehyde 3-phosphate and
dihydroxyacetone phosphate"
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          /transl-table=11
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isomerase"
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LGHSERRQYHQESNDTLLQKMTALTQELGVVFC
IGETQAQYDAKQTLPLVIDSQLAVV
KKLIAEQPEVIDSLSTRLIAYEPVWAIGTKVP
TVSEVSATHQYIKQTLAGFADSL
NMTVLYGGSVNADNADSFADPMIHGALVGGASL
KAESFLAIVTAFSGSM"
gene      74165..74473 /gene="secG"
CDS       74165..74473 /locus-tag="Psysc-0066"
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          /locus-tag="Psysc-0066"

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subunit secG"
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/gene="nusa"
/locus-tag="Psysc-0068"
/gene="nusa"
/locus-tag="Psysc-0068"
/function="transcriptional
anti-termination Structural and
functional similarities between
RbfA, NusA, and other bacterial
type II KH domains suggest
previously unsuspected
evolutionary relationships between
cold- shock associated proteins"
/note="Both RbfA and NusA are
regulated in the same E.coli
operon.; Citation: Carlomagno MS,
Gene. 2003 Apr 10;308:115-28.
PMID: 12711396 [PubMed - indexed
for MEDLINE] 2: Huang YJ, J.
Mol. Biol. 2003 Mar
21;327(2):521-36. PMID:
12628255"
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factor"
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GAQLLLSRTHPEMLSALMQKEVPE
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LTGYKLNMMLEEYQQRQANESKAFIELFYERLE
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VETFYDIEGLDDDAIDMIQERAKEVVIADLVKQ

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gene 74634..74717

tRNA 74634..74717

gene 74842..74918

tRNA 74842..74918

gene 75377..75877

CDS 75377..75877

gene 76010..77494

CDS 76010..77494

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gene	138792..139592	/gene="panB"
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CDS	144428..145138	
gene	145243..146130	
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/note="Citation: Brown L, Gentry
D, Elliott T, Cashel M (2002).
DksA affects ppGpp induction of
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Bacteriol 184(16);4455-65. PMID:
12142416"
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CDS complement(146719..1478 /locus-tag="Psysc-0125"
28)
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S"

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23)
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CDS	149143..151665	/locus-tag="Psyc-0127" /locus-tag="Psyc-0127" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="AAZ18001.1" /db-xref="GI:71037693" /translation="MSSTDITLTPSQTSINAQVLD ATTHANIHDKLARALGIKTAQVNA FVKLYDEGATVPFIARYRKEKTQNLDDAQLRALE KSLNYERDMATRRLLKIIELLSTQG NLTEELQTRIDNATSKLELEDIYLPYRPRRRSPA AKARAAGLDVAAQALLTQDVPTPD ALADYQVQSSITDESNEIEVDFSDIEKQLAGVQ AIIIVDEWTOALDLDLHLSRSSFAT ASIVSSVASEEKREVGKFKDYFEHSESLARLPN HRLLAHLRGRQENVLGLKIEGEDA PFIEKIIKHFAIDGKAPTERQEFLEAAASSLWKD KWRPHIEHRLLTEKRLTAEAAID VFANNLQHLMSAPAGRKVILGVDPGIRHGVKMA IVDAQGHVMLDGEDKPVIAIVYVF APDNKMTAKAVIDEELLSTYNVDLVAIGNGTASR ETDAMIKEILAANEALKAKAVIN ESGASVYSASELATDELGNLDSVRGAVSIARRL QDPLSELVKVDPKAIQVGOYQHDV NQTLQADSLDKVTQDSVNAVGVVDVNTASPAILAH IAGLNRNVAAQIIVTYRKEHGAFFDS RESLKNVPRLGAKTFEQAGFLRIHDGNSPLDAT GVHPESYKLVNDLLTQDKLSLPEV IGNDGVLSNIDITALAANDENVSVKAILDELAKP ARDPRPEFKTANFRDDVNSIKDLS EGMILEGVVTVNTAFGCFIDVGVHQDGLVHISQM ANDEVADPMNRVKPGDIVSVRVIS IDEKRRIGFSMKPEAEKFAAPAAKPAKAVTNN DEKTSRFRSNRPAQDKRPSKPKRQ PSSSNHSDSRKAPRAEKAEAFSKMGTFGALLQE AGVTAKAK"
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gene	167146..167811	/locus-tag="Psc-0140"
CDS	167146..167811	/locus-tag="Psc-0140" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.990) with cleavage site probability 0.982 at residue 24" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18014.1" /db-xref="GI:71037706" /translation="MWNNTLQILMVSTIMAVGVS LSACDNNKSGEVSAAEKVSADKQIV SDTPKPKTPAPNADLDGATVQEGTPVKYDVASWG PKKVEPLRVDQLDDIKSILGKVVS TDKNSLDYASNLASKYRFMNTEAPYLDLIDSEKY LELGWYFANPTDSDKEKKLSQNH KKSYYQLARQLMGDEGGKLVLADILSGQIINKNVIG GQKVELAKCEFYSCMMLINKSASQ NSK" /locus-tag="Psc-0141" /locus-tag="Psc-0141" /EC-number="4.1.3.38" /codon-start=1 /transl-table=11 /product="aminodeoxychorismate lyase apoprotein" /protein-id="AAZ18015.1" /db-xref="GI:71037707" /translation="MQPSNSWVCLSALEKQVVA TASLDNRGLAYADGFFTTMGVING QILWAEYHHQRLISHAKALQLDLSWSLLSTLQV HAQQHRQGMLKLIITRAAQDIRGY GYTPSECGSACESWLKSLAMTVSTAEQLSLNDEC SIPVQPVSTAVCLSSQIACLPSSI AGLKTILNRLDNVLASAELQGIKTRVLASNGEDI SEGLLRDMTGRWVEGTMSNVFYQL SDSRLVDSPSSEMINIPNNKSNNTNYLTQGGWYTP SMAQSGVAGVMRQVIIIDELSTTKY PVVVRSLQDKDLPLQLQQLFFCNALRGIMPASLT LLSGEMVGF"
gene	167815..168774	
CDS	167815..168774	
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gene	complement(169265..170029)	/gene="dnpC"
CDS	complement(169265..170029)	/locus-tag="Psysc-0143" /gene="dnpC" /locus-tag="Psysc-0143" /EC-number="3.1.21.4" /function="Recognizes and cleaves methylated sequences." /codon-start=1 /transl-table=11 /product="putative type II restriction endonuclease DpnI" /protein-id="AAZ18017.1" /db-xref="GI:71037709" /translation="MNLHFNQSLAKSYKSPSQIV RVLSEDWVAKQSYCPNCSAEPLVE FANNQPVADFYCGHCSEYEKSKKAKLSNIIND GAYDTMIERINSNNPNFFFLTYS QEYRVNNFLIIPKQFFKPDMIKRRKPLSMNAKRA GWVGCNIDLRKVAESGKVFLVKDQ QVIPRDNVTKQFKTLFLRAQSITSRGWTLDLVQ CIDKLEANFSNLQVYAFEAALQPK HPKNNHIQDKIRQQLQVLRLDKGIIIEFLGRGHYRK LY"
gene	170201..171484	/locus-tag="Psysc-0144"
CDS	170201..171484	/locus-tag="Psysc-0144" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="AAZ18018.1" /db-xref="GI:71037710" /translation="MSIPTPETPPERNDTLNSND QKGTADERVDGTPLNKSPVDEIGA KEVPTDISLISGDNKPRHYKIDNPSFFMQRGYQ VLLVLGLIAAFFLVMVYQTLFGRI EQPQQMVITIEGQTYYGLLPQWQOEIPLFSATIA KLYMKIQVDGGLHAGIYQLPENPT IAEALHVLGGQVKAAMVKVQIEGKTSKDLYQAL RDNKGIKKEVLTADSTNASIAQAL DLVGILPDTIVANSNDP IVNNHLEGWFAPDTYYYG EGTDDKKVLTDLKRRQQQALTKAW ENRAPNLPYQSPYEALVMAISIEKETSVEEERPL VSAVFNNRLNKSMMRMQTDPTIIYG MGSRYEGNIRRKDIDEKTRINTYQIDGLPPTPIA LPSAASIEATLHPAKSEALYFVAT GNGGHKFTNSLIEHNQAVKEYLGMVREKKAQTPP Q"
gene	171585..172262	/gene="tmk"
CDS	171585..172262	/locus-tag="Psysc-0145" /gene="tmk" /locus-tag="Psysc-0145" /EC-number="2.7.4.9" /function="Phosphorylation of dTMP to dTDP" /codon-start=1 /transl-table=11 /product="thymidylate kinase" /protein-id="AAZ18019.1" /db-xref="GI:71037711" /translation="MSASIQAPFSQTTTTPLQGH FISFEGTEGVGKTTAIEQLCARLQ ANGIDYLRTPREGSPFAERLREILLDPNTAIND

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CDS complement (172382..1746 73) /locus-tag="Psyc-0146"

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RSVPRNKTIISNLKWEIGIIPIG
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PKFPRDTILEFNESLTILLVSVLF
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/function="Degradation of polypeptides"
/notes="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.993) with cleavage site probability 0.989 at residue 47"
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VTLNDRTELDA TLVGS DERSDVAV
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DYSASAGIVSAKSRNFSRETSVSF
IQTDVALNPNGSGGPLFNQRGEVIGINSRIFSGT
GGYMGLSFSIPIDAAMDVYEQKLA
NGKVERAYLGIYPQIDIRNLAEAYNLARPQGALL
TRVSPDSPAQKAGLKSGLDIIILRYN
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gene 175485..176942

CDS 175485..176942

		ISLGLALRNLTPEEQVELASDNKTGVLVTAIEPT GLAARSGILAGDIIITNLHQKSIKT VNDVSSAVSVLPKKGVVTIEVMRQGPIGPIGLRI E"
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gene	178400..178735	
CDS	178400..178735	
gene	178866..179579	
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gene	complement (179656..1799 97)	/locus-tag="Psyc-0151"
CDS	complement (179656..1799 97)	/locus-tag="Psyc-0151" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18025.1" /db-xref="GI:71037717"

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AKKIKEARKDS"
gene      180101..180364    /locus-tag="Psyc-0152"
CDS       180101..180364    /pseudo
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                                /note="Methylpurine-DNA
                                glycosylase is a base
                                excision-repair protein. It is
                                responsible for the hydrolysis of
                                the deoxyribose N-glycosidic bond,
                                excising 3-methyladenine and
                                3-methylguanine from damaged DNA.;
                                Probable methylpurine DNA
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gene      complement(180969..1811
90)       /locus-tag="Psyc-0154"
CDS       complement(180969..1811
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gene      complement(181933..1821
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CDS       complement(181933..1821
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gene      182604..182855    /locus-tag="Psyc-0157"

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gene complement(182842..184173) /gene="dada"

CDS complement(182842..184173) /locus-tag="Psync-0158"
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TFSADSYVLALGSYSVALMKPLKI
HLPFPAKGYSATYQINPRAPHLAPFVSLIDDEF
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CDS complement(184228..184995) /locus-tag="Psync-0159"
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RPK"

gene 185292..185645 /gene="phnA"

CDS 185292..185645 /locus-tag="Psync-0160"
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PhnA is a novel carbon-phosphorus
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gene is part of a large operon in
Escherichia coli associated with
alkylphosphonate uptake and
carbon-phosphorus bond cleavage."

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		/locus-tag="Psyc-0161"
CDS	185744..187045	/gene="hemL"
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gene	189235..190038	/locus-tag="Psyc-0163"
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CDS 190316..191893

gene 192082..192915

CDS 192082..192915

gene 193038..193607

CDS 193038..193607

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		/locus-tag="Psysc-0167"
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gene	194905..194994	/locus-tag="Psysc-R0003"
tRNA	194905..194994	/locus-tag="Psysc-R0003"
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tRNA	195179..195255	/locus-tag="Psysc-R0004"
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gene	195455..196129	/locus-tag="Psysc-0168"
CDS	195455..196129	/locus-tag="Psysc-0168"
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gene	complement (196376..1967 56)	/gene="pand"
		/locus-tag="Psysc-0169"
CDS	complement (196376..1967 56)	/gene="pand"
		/locus-tag="Psysc-0169"
		/EC-number="4.1.1.11"
		/function="Alanine synthesis"
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		/product="putative aspartate 1- decarboxylase"
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		/db-xref="GI:71037734"
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gene complement(196856..197437) PRLVYCNEEDNTVKDTANIIPVQVA"
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/locus-tag="Psync-0170"
/EC-number="3.1.1.29"
/function="Peptidyl-tRNA hydrolase (PTH) is a bacterial enzyme that cleaves peptidyl-tRNA or N-acyl-aminoacyl-tRNA to yield free peptides or N-acyl-amino acids and tRNA."
/codon-start=1
/transl-table=11
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IKLKTIDGGHGGHNGLRDITPHIGNDFHRLRVGIG
HPGHKSKVSGHVLKAAAPDEQIAI
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gene complement(197634..198308) /locus-tag="Psync-0171"

CDS complement(197634..198308) /locus-tag="Psync-0171"
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GQKINMNVVHFHSGREEAPGTKAGGILSTLVTDI
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LFRLSDIKLEPGVLIIFDLDMEDAHDRITVNMQPP
TVQEVDKVAEIDASDVPATEQGTID GNKDGK"

gene complement(198705..199652) /gene="prsa"

CDS complement(198705..199652) /locus-tag="Psync-0172"
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/locus-tag="Psync-0172"
/EC-number="2.7.6.1"
/function="Pentose Phosphate Pathway -> Histidine biosynthesis, pyrimidine biosynthesis, and purine biosynthesis"
/note="Produces 5-phospho-alpha-D-ribose 1-diphosphate, a precursor for histidine, pyrimidines and purines."
/codon-start=1
/transl-table=11
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GFFDIPVDNIYGTPVLLNDLQKQN
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 RRARANESQVMHIIIGDVRDRDCVI
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gene complement (199763..1998 /locus-tag="Psc-R0005"
 38)

tRNA complement (199763..1998 /locus-tag="Psc-R0005"
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gene complement (200082..2001 /product="tRNA-Gln"
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gene complement (200407..2013 /product="tRNA-Gln"
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 GSSNAATTLLVLNEIWQLNFNQE
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 DLDPQQYLVLTENAHVNTAKLFAH
 EKLPFDITLLSIEITIKNQYDNIYVQTLIAPYHNVF
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gene complement (201438..2020 /locus-tag="Psc-0174"
 76)

/note="Signal predicted by SignalP
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CDS complement (201438..2020 /locus-tag="Psc-0174"
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gene complement (202218..2038 /locus-tag="Psc-0175"
 82)

CDS complement (202218..2038 /locus-tag="Psc-0175"
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GIYPNSDDDKRELLSALQPIASEK
NASLSVLKAGLLYQFNEPEIAIIHINHALEQQPD
YVPFITLKADILRKIETPKAVLDH
LSQAHLRNANSKNLYLYEIRYLLDLKQNEQAWQL
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RKVVALLDLDNDVDAATATLEKMRDFSVPFAPS
FVLQADILWQQNEGAELLLTKA
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SEQGLALATAIIQIRYDDPRYDNERHLQALNVLA
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WLADFQKLSLDEIDPYLYVHRDMHALTHWLRVAA
GLDSMILGEPQLIGQIKRAVHLAQ
DQKALSNQLGWIVDQVFAAKVRVNETQVGAQAV
SLSYAAAKLVTIQIFDDLPSTRLLV
VAAGEMNRLVAMHIAAGLVGRIIICNRNPERAEA
LAELRNPKRQIEVRTLQELPQVL
AEADIVSSCSGSDMILIDKMTLRLALKSRRYQPM
LMIDLAVPRDIDSTVSRIDDVLY
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CDS       206442..207578
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metabolism"
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IVYAPHVETSSGIILSEEYIKALS
EAVHSVGLLVLDICIASGCVWDMKELGIDVLIS
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PTDSLQFRDAILEAKEIGFDILR

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gene	207814..208251	
CDS	207814..208251	
gene	208344..208766	
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gene	complement(208866..210530)	
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gene	210870..213005	AHETPKVTIASAK" /gene="fadH2" /locus-tag="Psync-0181" /gene="fadH2" /locus-tag="Psync-0181" /EC-number="1.3.1.34" /codon-start=1 /transl-table=11 /product="2,4-dienoyl-CoA reductase" /protein-id="AAZ18054.1" /db-xref="GI:71037746" /translation="MTASHTANSIDTASLNHYP HLFEPDLGLGFTTLKNRLVMGSMHT GLEDRFYNYGKLAAYFAERAKGGVAMMITGGISF NREGWLLPASGTMNTRADVLNHQR VTRAVHKYDSKIIMQILHSGRYGYHFFVSSSPI KSPISPFKPRKMSIKNIEQTVKDY ARSAKLAKQAGYDVGVEIMSGEYLLNQFLSRHVN KRTDEYGGDIQGRMKLAVDVVKAV REAAGEDFIMLFRLSVIDLVDKGNVMDEVIIVAK ALEEAGVTIMNTIGIGWHEARVPTI VTSVPRAAFVDFTAIEIKKHISIPMAANRINMPE TAEIIVASGQADLIQMARPFLADA HWVNKAKDQADRIINTCIACNQACLDFDNKRS TCLVNPQACYETELVYKTKKPRK VAVIGGGVAGMSAAHVAALRGHEVTLFEAKDILG GQFNYAKVIPGKEEFFETIRYYIN ELEHLGVEIKLNTKVDKAMLEKAKFHHVIVATGV VPRSLAGKLEGADLPQVMSYALL SGEKSVGATVAVIGAGGIGDFDVSEYLTAKHGQPL DELDPPELLKDDSYRPFKAQSIIEWR EEWGVTSATDYQTEGGIITKGDITPVQVYLIQR TKRGLSGSLNKTSGWVHRAHVKSH GVIVQSGAQYDKITNEGIWITNNQGSQLLRVDS VVVCAGQESVVELMENVGDAPDAQ YHLIGGAKLAAELDAKRAIRDGAEVAASI" /gene="nemA" /locus-tag="Psync-0182" /gene="nemA" /locus-tag="Psync-0182" /codon-start=1 /transl-table=11 /product="putative N-ethylmaleimide reductase" /protein-id="AAZ18055.1" /db-xref="GI:71037747" /translation="MAHDNLFEPVKMGQTILKNR IIMAPLTRLSVEPGDVPTALASE YYAQRSGAGLIIEATQVFSQAKGYAGAPGIHTE EQMTAWKTIIVDNVHAKGCKIVVQL WHTGLVAHESVQPDGKAPISASDVNVGVRTSLRD SNNQAIRVDATTIPRPATLEEIQV IADFLGATKNAKEAGFDGVEIHGAHGYYLLHQFVV EHTNQRTDEYGGSGRENARLMLAV IDACVDAWDADHVIGIRISPLGTFFNNVEAGYNEDE NIWLIQINQRLMYLHLSEPDWA GGTPYSTEFRQRVREAFGQMIIAAGGYTAEKAE NIKDGYIDAVAFGRDYIANPDLA RIRREGAPLNEQHPSFYGGGTGYDYFPLNQA" /locus-tag="Psync-0183"
gene	213389..214492	
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gene	complement(214749..2160 65)	
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GVCNGCQMAQLKDLIPGANFPR

gene	225212..225685	FIANKSARFEARTVNVKVERTKSILFKGMQDSIL PIAVAHGEGYATLDNTEIDGMAKH GQLAMRYVDSQGHPTETYPINPNHSGSLGGVTGLCS TDGRVTIMMPHPERTLRAYNHSWK PEAWDEDGAWMMRMFNARNAVRW /locus-tag="Psyc-0188" /locus-tag="Psyc-0188" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="AAZ18061.1" /db-xref="GI:71037753" /translation="MGSYIDSNLITNERVIKEAQ VSWWSQWPFVIGGLFLLSGMGAS LAPNEDGGAGVILFIASVFIFAIIRVISTELAL TTKRVIATKGFIRRNITIELRLKLV EGFVNVQSIFGRIFNYGSVVSVGTGGIKTPIPI YNPAEFMVVNEFLNENPSQFD" /locus-tag="Psyc-0189"
CDS	225212..225685	
gene	complement(225740..2274 97)	
CDS	complement(225740..2274 97)	/locus-tag="Psyc-0189" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18062.1" /db-xref="GI:71037754" /translation="MSTESIIISLIVFFLLIAFI RHVVYPLVIDSYFKGTFKFLAVKAR VQQHIDECNELNEHIEHLKLSYTYAEATDYGEGL LSDASRYNMKRRTWATESSDNRWT HNCSASIVKSADNPQYKYLCKYFNISPNKETLEQ FEEVLNNSFAVEQKGYLLENAREA IVSSITSLSPLYLRHYDRVRNTELGFKKISLSN LYFPVYTRYASAGNKSNSFALE LNLDRLERFIGYLANLLKVKNSVAGQRALMTAKL REEIKERDSYACKICNLSTSDAN LLEIDHIIPLSKGGVTCESNLQTLCKWCNRSKG SKIYSADVIPNPAITDSRKLDITW EPKASTPTDSGKLDMPKASTPTITGLQSSSTFE DGRTRNAMTKQGTNLTIRPQANALR SAKDYEYSYGYSRKGLIEQLHECDDYVVSATVA VDSLNIIDWKEQAVKSAKDYIEYSG YSRKGLIEQLHECDDYVVSATVAVDLSNIIDWKE QAVKSAKDYIEYSYGYSRKGLIEQL HECDDYVVSATVAVDLSNIIDWKEQAVKSAKDY EYSYGYSCKGLIEQLHECDDYVVSATVA ATYGAEQACLFVASLTSKN" /locus-tag="Psyc-0190" /locus-tag="Psyc-0190" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18063.1" /db-xref="GI:71037755" /translation="MTTQSDIKKHIDQITIPASVQ AQSQEQRIKELERENKELQANEI IRKAAAFQAQELDH" /locus-tag="Psyc-0191" /locus-tag="Psyc-0191" /function="Folate synthesis" /codon-start=1 /transl-table=11 /product="possible alkaline phosphatase" /protein-id="AAZ18064.1" /db-xref="GI:71037756" /translation="MHQMSWVLAIMANFGYGLI IFAMFAENVFPPIPSSELIMPAAGF AAARGDLNILLVIVAGTFGSVLGALPLYLGTFL NKERLIVFTEKYGYKVFIKESDVL
gene	227710..227889	
CDS	227710..227889	
gene	228171..228800	
CDS	228171..228800	

SSNAWFDKHGKAVFFGRMVPGIRSLISIPAGMN
 KMPLLSFLVLTALGSSIWITMLTL
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 LIKRRLSAQHNSNNI"
 /locus-tag="Psyc-0192"

gene complement (229127..2292
 67)
 CDS complement (229127..2292
 67)
 /note="High homology to COG3328,
 yet very short sequence."
 /codon-start=1
 /transl-table=11
 /product="putative transposase and
 inactivated derivatives"
 /protein-id="AAZ18065.1"
 /db-xref="GI:71037757"
 /translation="MTVFFNYPKDIRKAIYITNA
 IESLNSVIRTAVTKRKVSLLIRQH SR"
 /locus-tag="Psyc-0193"

gene complement (229310..2308
 66)
 CDS complement (229310..2308
 66)
 /note="contains a TerC, 2 CBS and
 1 CorC domains"
 /codon-start=1
 /transl-table=11
 /product="probable transport
 protein, TerC family"
 /protein-id="AAZ18066.1"
 /db-xref="GI:71037758"
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 EIIILGIDNLVFFIAILANKLPFHQR
 TKARNLGLGLAILMRGLGLEFVMSWLVTLTEPVVS
 YATFNLSIRDILILVGGFFLLLLKA
 TLELHERLEGLKDANNNSKVYAGFAAVVAQIVIL
 DAVFSFDAVITAVGMVEHLEVMMMA
 AVIVAMAMVLAALAKLTDVFGKHPTVIVLCLSP
 LMIGFSLIVEGLGFHPIKPSYLYAA
 IGFSVIEAFNQFMQRNRKTHESAIPLRDRTADN
 ILRLMGGKTSNNDEELLADETS
 ESIPTFAEEERYMISGVLAALGERDVETIMTPRSEV
 SWNVNEDDLKEIREQVLSSTPHSL
 PICQQLNKILGVVRAKDLAVLDEQPNNIYAL
 EPLLTQQQPVFVSDIIDLNLRLNL
 LKNAKGNLAIVVDEYGGVAGLVITPLDLFEAIA
 GEPDEETLEIVKQEDHWIAEGTIS
 LDQLRLLELNDPSSLGAEQLTIGGYINFKLDGIA
 QVNEHVSSDGFIFTVLETLSTRIL
 LVKIERDVAQ"
 /locus-tag="Psyc-0194"

gene complement (231329..2317
 42)
 CDS complement (231329..2317
 42)
 /note="Member of bacterial family
 of proteins related to iojap from
 plants. The gene iojap is a
 pattern-stripping gene in maize.
 RBS found."
 /codon-start=1
 /transl-table=11
 /product="conserved hypothetical
 protein"
 /protein-id="AAZ18067.1"
 /db-xref="GI:71037759"
 /translation="MTNTMTDERLQECILTVENA
 LDDMKAKNITIMDVAALTDVMERI
 VIADGTSKRHVRAADSVGAAGKQAGFMPLGREG
 GIDSDWTLIDLGAUVVHMMTPQAR
 EFYDLEGLWSSPEQLAELVAVPREKKTAGRRNKN
 K"
 /gene="nadd"

gene complement (231882..2327
 66)

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CDS      complement(231882..2327 /locus-tag="Psc-0195"
66)      /gene="nadd"

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        /function="NAD synthesis"
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        /transl-table=11
        /product="nicotinate-nucleotide
        adenyltransferase"
        /protein-id="AAZ18068.1"
        /db-xref="GI:71037760"
        /translation="MLNIANNHNSQISKAIRAY
        LGGSFDPVHNGHLQAMMYVVEYLL
        PIAEQQRPLYVSLLPNARSPPKSNSTNPEHRLA
        MLKLTATQESPLYINELELWQVPPV
        YTIDSVQTLRARYPNDSLIFIMGDSARSLEQWK
        DGLQLTDYVNLWVFNRKNSDINK
        RFSETNLQTLKSQLPVLLQSTINSPAEVLTLT
        SRNITDSTILKNAYQGRIYLDPRP
        VAAISSTQVRQQLRQPLPQAPQSLNKHSAETQI
        ASLQPIINDIIGNTAPNSLAKWLNLP
        AVYQYIIAHQLYSAAQFR"

gene      complement(233099..2352 /locus-tag="Psc-0196"
55)

CDS      complement(233099..2352 /locus-tag="Psc-0196"
55)

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        /protein-id="AAZ18069.1"
        /db-xref="GI:71037761"
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        LDKQNSLDSSSALAMHAFGLKPKPSISRQHVEM
        IGDNDLDDLMEEVVVVYHTLGGDY
        DVVCEGLVPTTETSYSASQINRAIAHALDARIIF
        VSTADTSKPAYLADKLDVHAREFG
        GMASDRMLGCILMRHDLPTQSTLENQIVAPGE
        AIVSLDSGFIQEVQRLSPHENSEQ
        FRLIGVVFPSDSLSPVRTWDIAELDATWLNVG
        AKSRRINRISLTARSVARVDEVFK
        RGTLLVVPVGGDRDDLAAAGLACINGVPLAGLVLT
        GGVLPSSVVAELWQSAKLTGIVFM
        SVETDSYETVQNLVHMSAEIIPSDTERAEVARY
        VAAHLDLSWIKAYFSQNHEPRLSP
        SAFRHQVVKKAQIAKKRIVLPGESEPTVEAACI
        CQSRGIANCVLLAKRSDEQVAKN
        RDLVLPGLEIIDPDSLDMSKYIAAVVERRKGKT
        SAEVAAEYLQDTVYLGTTMLQMD
        VDGLVSGAHTTANTVRFAPAFQLIKTAPEYSLVSS
        IFFMLLPEQVVVYGDAINPNPA
        EELAEIAIQSAQSAAFGIDPKVAMISYSTGSSG
        MGADVEKVTRATQIVRERAPNLKV
        DGPLQYDAASVMSVGKQKAPDSPVAGQANVFIFP
        DLNTGNTTYKAVQRSANVSVSGFM
        LQGLNKFPVNDLSRGALVDDIITYIALTAIQAHSD
        VI"

gene      complement(235349..2365 /locus-tag="Psc-0197"
81)

CDS      complement(235349..2365 /locus-tag="Psc-0197"
81)

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        /product="acetate kinase"
        /protein-id="AAZ18070.1"
        /db-xref="GI:71037762"
        /translation="MSAGVTTTFDDKHSESTLT
        NPTLVLCGSSSIKALISDDETT
        RITGLAENLGLDTARIKHTTLNGEKLIAIAGGR

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gene	237088..237513	/locus-tag="Psyc-0198"
CDS	237088..237513	/locus-tag="Psyc-0198" /note="Two transmembrane helices predicted." /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18071.1" /db-xref="GI:71037763" /translation="MVIFYLYVGVFFIRASTGIV SIKKILALSNHCSIKGFYSMFNTQ RTSNKQRSNSRLSASRHGVYTLIFGTSIVIASVT LVGCGQKGNLYLVDASSKAVQDST AILDSGSNPQDTAFKIDGDQKNTEDFQLPEPSN DPNDY" /gene="lysA" /locus-tag="Psyc-0199" /gene="lysA" /locus-tag="Psyc-0199" /EC-number="4.1.1.20" /function="Lysine biosynthesis via the diaminopimellate pathway." /codon-start=1 /transl-table=11 /product="diaminopimellate decarboxylase" /protein-id="AAZ18072.1" /db-xref="GI:71037764" /translation="MSQSVITQTEQGLYNPEAL TAHLPALHYQNDALHMEQVSITEV VKHYGTFCFVYSKQAILAVYQAYTDSFASLNHQT CYAVKANSNLAVLGVLAQAGAGFD IVSRGELMRVLAAGGEASRVVSGVGKTSYDIEY ALNQSIGCFNVESISELTILINDVA KALDKSAPISLRVNPVDVAKTHPHYISTGLKDNKF GIAHEDALVYVYQAAKLSHINIVG IDCHIGSQLTEVEPFVAALDKVIELVHSLGKVGI ELRHIDLGGGLGVRYIDETPVSID EFANALLPKLSKGLTGVFFEPGRSIVANAGILLT QVDVLKPTTEHKNFATVDAAMNDLI RPALYQAEMAVIPSALPNNGIDTEGTQPWDIVGA ICETGDFLAKDRLLSLATGDVLA TGAGAYGFTMSNYSNRPRASEVMVADDRHQLIR KRESIEALYADEVLWQ"
gene	237623..238954	
CDS	237623..238954	
gene	239291..240178	
CDS	239291..240178	/gene="dapF" /locus-tag="Psyc-0200" /gene="dapF" /locus-tag="Psyc-0200" /EC-number="5.1.1.7" /function="Lysine biosynthesis via diaminopimellate synthase" /codon-start=1 /transl-table=11 /product="diaminopimellate epimerase" /protein-id="AAZ18073.1" /db-xref="GI:71037765" /translation="MLIEFTKMHGLGNDFMVIDL VTQRLDLTKDLVQLLGDRLHIGIF DQLLVVEPPMRPDVDFSYRIFNTDGTETEVCQCGN

		ARCFARFVQARKLSFKQRLRVETA SGIISLTTDHYGWVEVDMGPKPFEPSEIPFTTPRA TTKIQNAYHLDVNGTPVLVYANM GNPHAVIKVDDVLDADVESLGRAIESHPAPPERV NVGFMQVMNQRIHRLRVYERGVGE TQACGTGACAAVAIGIREGWLDEGEDVRAQLYGG SMVIKWPQGYSSMMTGPATFVVEY VFSPDGLMAQAGIKPNPEI" /gene="xerC" /locus-tag="Psyc-0201" /gene="xerC" /locus-tag="Psyc-0201" /function="Possible site-specific recombinase that acts on cer sequence of ColE1, effects chromosome segregation at cell division." /codon-start=1 /transl-table=11 /product="tyrosine recombinase XerC subunit" /protein-id="AAZ18074.1" /db-xref="GI:71037766" /translation="MVMSYTNPHVTDASQSDSPSW LSAELALTIEDAAALRELLAPVHR WLNVLVSVRNHSPHTLTAYFAGLNQLALFLRGKCL TWTRCDKROLAQHISQRLDEDKLA LASVQQLSAIRHFYGLWIEEDLARINPTTGYYL KRSPRPLPSIADVDLLTQLLDQEI PDTPEQARLWLRDKAMFELLYSSGLRVGELVALD IADVDLADLRVRVTGKGNKTRLVP LGIKAADAIRRYLPHRNLWVEQMDTALFISEKLG TRLSTRAVQORLKVAAATRAGIAQN MYPHLLRHCFASHMLSGSGDLRAVQEMLGHSDIS TTQIYTHVDFAKLTQVYDRAHPRA THASKDSSTT" /locus-tag="Psyc-0202" /EC-number="3.5.5.1" /function="hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds" /note="Hydrolase conserved domain" /codon-start=1 /transl-table=11 /product="possible carbon-nitrogen hydrolase" /protein-id="AAZ18075.1" /db-xref="GI:71037767" /translation="MSNPINNQLTVAAIQMNSQ QNIEDNLADIKAAIEEAAAQGAQL AVLPECCSMGRQFATAEHFDALSAMIAEYARTY GMYVLASGLPCPYRPDGVIVPDGR LRQASLLFAPDGTRIARYDKIHLFTATVADKQGS YNEAATFEPGAQTVAALDVEGAV YQLGMMVCFDLRFPALSQLRQAGAEILLSAPSAF TYLTGQAHWSLLQLARALDSQCMV IGAQQGGEHAYKDGHTRTQWGTMTSAYDGTIVIS SYDASELNQSLNEDNKNYAIVLAT LDRQAQNGRQKMPIFDCHRLA" /gene="rpoN" /locus-tag="Psyc-0203" /gene="rpoN" /locus-tag="Psyc-0203" /function="required for the transcription of promoters that have a characteristic -24 and -12 consensus recognition element but which are devoid of the typical -10,-35 sequences recognized by
gene	240236..241273	
CDS	240236..241273	
gene	complement (241487..242383)	
CDS	complement (241487..242383)	
gene	242863..244572	
CDS	242863..244572	

the major sigma factors."

/note="contain all necessary domains of rpoN except conserved octapeptide with unknown function; Citation: Merrick M.J. In a class of its own--the RNA polymerase sigma factor sigma 54 (sigma N). Mol. Microbiol. 10: 903- 909 (1993) [PubMed: 7934866]"

/codon-start=1

/transl-table=11

/product="probable Sigma-54 factor family (RpoN)"

/protein-id="AAZ18076.1"

/db-xref="GI:71037768"

/translation="MSMSFGLATTLSISQKLTPQMQAIAIKLLQLSSLELAQEVQAKLDSNPILLERIEDDEEYEGADKSADKDALVEFGEPLTLDWNQNTASDTFSVSSSSNNDEFEFYDSDISDLDLKLQDDSDTDAIDSYMLEDGSGNEESLNYDSPYAEYDGFDTASAGTGSPGARPDSDDFDSYQGSNTATIQDHVRWQLNFKRLSETDLIAEYLMDSMDMGFVRLDIEELLQSFDTIASFYQWDERVEHDEVMAVLRMIQSCDPLGVGARNLSECLAIQLSKLDTDIPYLKQAQALLSASEHLVSNNIKALTERTGLAAQEITPALMLLRSLNPSGLLFQSRQPDYTSQSPDSYDIPDVLTPIRRHDANQNTDTSTQEDGWQVRLNPETLPLKRVNQEYANLVKRGDNPQNYLRENLTARLFIRSIERNQNLLKVATSVIRYQQAFLQYGATAMQPLILKVIADVDLHSTVSRLTSTKITLTPQGLFSLKHFFSSHVSDDGDISIAISAMIKQLIADPEPKPLSDSKIKNYLLAEGIDIARTVAKYREAMSIGSSQTK QKY"

/gene="yfiA"

/locus-tag="Psyc-0204"

/gene="yfiA"

/locus-tag="Psyc-0204"

/function="possible binding to sigma factor 54. implicated in biofilm formation in Bacillus and quorum sensing in P. stutzeri"

/note="encoded adjacently (downstream) from RpoN (Sigma 54); Citation: Heurlier K et al. J Bacteriol. 2003 Apr;185(7):2227-35. PMID: 12644493 [PubMed - indexed for MEDLINE] 2: Oosthuizen et al. Appl. Environ Microbiol. 2002 Jun;68(6):2770-80. PMID: 12039732 [PubMed - indexed for MEDLINE]"

/codon-start=1

/transl-table=11

/product="SSU ribosomal protein S30P / sigma 54 modulation protein"

/protein-id="AAZ18077.1"

/db-xref="GI:71037769"

/translation="MNVISGHHISITDAMDTAVREKLEKVERHFDRIQSLQVILSLD NSGAKKSHKAEAIMRVSGKEMFVQALDDMYKAINEMADKLDRQVRKYTKLESKKTQ GAGRDGRYEDLMTAEAPAVEAAV"

/gene="this"

/locus-tag="Psyc-0205"

/gene="this"

gene complement(245787)..245987)

CDS complement(245787)..245987)

/locus-tag="Psc-0205"
 /codon-start=1
 /transl-table=11
 /product="possible sulfur transfer protein involved in thiamine biosynthesis"
 /protein-id="AAZ18078.1"
 /db-xref="GI:71037770"
 /translation="MSNISVNGKKLQTHQTVQLVVNELGLSNGRYAVEVDGELIPKSELDRLHIVEGMTIEVVQAVGGG"
 gene complement(246097..246471) /locus-tag="Psc-0206"
 /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.984) with cleavage site probability 0.416 at residue 25"
 CDS complement(246097..246471) /locus-tag="Psc-0206"
 /note="Signal peptide and 4 transmembrane helices predicted. RBS found."
 /codon-start=1
 /transl-table=11
 /product="conserved hypothetical protein"
 /protein-id="AAZ18079.1"
 /db-xref="GI:71037771"
 /translation="MIMLNWISIAINMAIAVALGAFGAHGLKAMVSTQQLLEWQATATLYWVFVHSLGLLLVGILIRLNATTAALLQIGVIFAGSLYAMTLGAPRWFGAITPIGGVLMIAAGLWLALSSARLTNS"
 gene complement(246530..247555) /gene="rpoH"
 CDS complement(246530..247555) /locus-tag="Psc-0207"
 /gene="rpoH"
 /locus-tag="Psc-0207"
 /function="DNA binding (GO:0003677) transcription factor activity (GO:0003700) DNA-directed RNA polymerase activity (GO:0003899) sigma factor activity (GO:0016987)"
 /note="contains the sigma 70 domains 2.2 necessary to bind to core polymerase and 4.2 necessary to bind promotor; Citation: PubMed=6088062; Landick R., et al.; Nucleotide sequence of the heat shock regulatory gene of E. coli suggests its protein product may be a transcription factor.; Cell 38:175-182(1984)."
 /codon-start=1
 /transl-table=11
 /product="putative Sigma 32 (RpoH)"
 /protein-id="AAZ18080.1"
 /db-xref="GI:71037772"
 /translation="MANTITNAANTRRKDSAAPEKNEAREAAALKAAAERPPYDASALGDTSTRDLVPAMPHTLSAPGVNLGAYINTVHQIPI LTPTQEQELAHRYIDEQDVAAARL LVMSHLRFVVIHARSYSYGYLPQADLIQEGNLGL MKAVKRFDPNKGVRVLSFAVHWIK AEIHEFVIRNWRIVKVATTKAHRKLFFNLRLSLKK TNNQLTIEADAIAANDLNVTRKQV LEMESRLTSYDASFEAQSSDDDDGRYAPQLFLED GIDPAEIVEESDWEENNSSALIAA METLDDRSRDIVEQRWLSEQKSTLHELAAYYSIS

gene complement(247635..248102) AERVQRQIEKNAMDKIREAMTIDSV ILPDDIQ" /locus-tag="Psync-0208"

CDS complement(247635..248102) /locus-tag="Psync-0208"

/note="RBS found."
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/product="hypothetical protein"
/protein-id="AAZ18081.1"
/db-xref="GI:71037773"
/translation="MSADSPSIMVRASYPICLAE
TVSKSGQQSIQRLDLLPVPNDINL
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LRSSVVGESLYVVAATPNSQADIM
AFCQQSLQTDENPLSLIINQATVSDSKAASDNQ
TKYSVDTIYHFIIITKTDN"
/locus-tag="Psync-0209"
/locus-tag="Psync-0209"
/codon-start=1
/transl-table=11
/product="conserved hypothetical protein"
/protein-id="AAZ18082.1"
/db-xref="GI:71037774"
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TRALKLAVSTILLACTSAAYSKSQAPLSDDSWQ
TTGTALNPLNLRGQGLSFEEQYQ
NKLGLWESLRNNGRVKMEHDPWQIETVKELTWR
LNAQARQQAPLGLVINDPNSINAF
AAPGGVIGLNTGTILAANSMDLAVVVAHEVAHI
SQRHYESGADERKKALLMQIGGML
AAIAASTVDGDAAAAMMGSQTAAMNSSMAFSRN
NERDADRVGMQIMNQAGDYPRAMP
RFFTHNQKSMQNTANQFLPSFIRSHPLSNERL
SESQSRQRYNALPLNQQRHQAL
FDLLYWRVQSTGKHASEMALMTAAKNSVGAKLAL
MHVYGAQQRFKEADDLFVELSALS
IAKRQVLEPLLSITQSQILTEQNKWQAAEVLES
QQRLYFERDLRLYLAEALTNQ
ETKAQVLLKPLTEQQPSDRYAWQSLQLANEKLAK
TTDSAPLKSIAITINALRYRSHDQL
WSGHYERALTSLTQAKQLEKLQNTAQANSARPL
LANINAEIKAVKTAKDFK"

gene 248494..25179 /locus-tag="Psync-0210"

CDS 248494..25179 /locus-tag="Psync-0210"

/note="Possible GatB/Yqey domain (trRNA metabolism). RBS found."
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/protein-id="AAZ18083.1"
/db-xref="GI:71037775"
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LDDAEVLEILQKQLQRHESLTIFTENGRDDLAT
KEQFEIDIINEYMPKQMDDAELAA
LVSAETAEQGATSMRDMGSMGILKSKTAGRADP
ALISKLVKDALQG"

gene complement(251039..251254) /gene="rpsU"

CDS complement(251039..251254) /locus-tag="Psync-0211"
/gene="rpsU"

/locus-tag="Psync-0211"
/codon-start=1
/transl-table=11
/product="SSU ribosomal protein"

		S21P"
		/protein-id="AAZ18084.1"
		/db-xref="GI:71037776"
		/translation="MPAVKVENEPVDIAIRRFK RACEKAGVLSVVRKREFYEKPTQV RKRKKAAAVKRYKKLQRETITRMY"
gene	251670..252038	/locus-tag="Psync-0212"
CDS	251670..252038	/locus-tag="Psync-0212"
		/note="Signal peptide predicted; Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.603 at residue 31"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAZ18085.1"
		/db-xref="GI:71037777"
		/translation="MKTGIKKSUVVSTALWAILAL IMGVLSACSSEKEGEASEHILAV DRVDAALARKNAPAAEKMDPAPMPAVGAT TDATMSTEEGAUVVEGTAADATAS VDSIDTAMAPADSAMPATIN"
gene	252105..252626	/locus-tag="Psync-0213"
CDS	252105..252626	/locus-tag="Psync-0213"
		/note="Cytochrome c domain at c-terminus; Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.417 at residue 34"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAZ18086.1"
		/db-xref="GI:71037778"
		/translation="MTVKQSVIKKKSVVKLALSG LSLGSLLTSLACSAGDNTAADEPA AINETEAAATETVVVEPAAPTEAEELTAEAEVPAVE AEVVSAAEATDPEVLADAGATLY EKQCKVCHEKGLLAAPVFGNKEAWAPRIAKGIDT LHMHSAGKGNKMPAQASAEVSEAQ VHAADVIMVAASV"
gene	252902..253951	/gene="ygjD"
CDS	252902..253951	/locus-tag="Psync-0214"
		/gene="ygjD"
		/locus-tag="Psync-0214"
		/EC-number="3.4.24.57"
		/function="proteolysis and peptidolysis"
		/codon-start=1
		/transl-table=11
		/product="O-sialoglycoprotein endopeptidase"
		/protein-id="AAZ18087.1"
		/db-xref="GI:71037779"
		/translation="MKVLGLTSCDETGLAIFDS EQINSENGLLGQVLYSQIELHAL YGGVPELASRDHIRKLVPLFNELLAQCNIKDE IDAIAITKPGGLIGALMTGALFGR SLAYGLDIPAIGIHMEGHLLAPLMGLNPPAFFP VSLVSGGGHTLLIAAHGIGQYEIL GESIDDAAGECFDKAAKMLGLPYPGGPNIAKLA NGNPNAYSILPRPMLHRLDFSFSG MKTAVHNLKIDTSGNGSDSDPQVRADIAASFQ HAVVDTLVKKCKVALKQVDMSLRV IAGGVSAANSHLRETLERELAKINATVHYAPPALC TDNGAMIAIYAGYERLQAGQSDDLA VSCVPRWPMTELPV"
gene	254011..254382	/locus-tag="Psync-0215"
CDS	254011..254382	/locus-tag="Psync-0215"
		/codon-start=1

		<pre> /transl-table=11 /product="camphor resistance protein CrcB" /protein-id="AAZ18088.1" /db-xref="GI:71037780" /translation="MQWLAIGLGAAGACLRGWL ARFNPLHHWIPGLTGANVVLGGLL IGLALVWFERMGSGLSPNIRLFVITGFLGLTTF STFSAEVFTFIHHGRLLAALGLVG LHVGMTLLATALGFYCFKLVL" </pre>
gene	complement(254413..255303)	<pre> /gene="metr" </pre>
		<pre> /locus-tag="Psysc-0216" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.817) with cleavage site probability 0.371 at residue 24" </pre>
CDS	complement(254413..255303)	<pre> /gene="metr" </pre>
		<pre> /locus-tag="Psysc-0216" /function="The majority of these proteins appear to be transcription activators and most are known to negatively regulate their own expression." /note="All possess a potential HTH DNA-binding motif towards their N-termini." /codon-start=1 /transl-table=11 /product="putative transcriptional regulator, LysR family" /protein-id="AAZ18089.1" /db-xref="GI:71037781" /translation="MLELRHLNLTALRAHGSIA AAADELHVTASAVSHQLKELENY DISLVNRRTRPLTFTPAGKTVLALADSI MPQVAR TKANLKRLAHGQAGRLRLASECHS CFDWLMPILNYYRREWSDELDFATGFEP PHHL LMEGDIDLLITTSNLP IEGISYQP LFEXESRLVLSFTHDLAEQHF IHPNDL IEETLIA YPVEAKRLDIIANFMTPEQVSFKA IRTELTAMLIQLVASERGVAAALPDWV VVAEYK GWVVSRLGDSGYCQLYAAATRSSS QDTAYMQGFASLLEGIVKPV" </pre>
gene	255969..256607	<pre> /locus-tag="Psysc-0217" </pre>
CDS	255969..256607	<pre> /locus-tag="Psysc-0217" /EC-number="4.2.1.1" /codon-start=1 /transl-table=11 /product="probable carbonic anhydrase" /protein-id="AAZ18090.1" /db-xref="GI:71037782" /translation="MPHDTRLQTGLEALALLK QG NVRIVDSLTSTDPICQRRPELVSD QDPVAIILGCSDARVPVEIVFDQGLGDL FVIRVA GNVVPASQIGSVFAAEKFGTKLV VVLGHSCHGAVTACVEALINPEKNYSPN LQSI VD RIRPSVYNLHELATANGQDVDADE LVDRSIRANVHMSVSQKLKHGSRALEDL TSSGQLL IVGAEYDLETKVRFELDA" </pre>
gene	256690..257259	<pre> /gene="gloA" /locus-tag="Psysc-0218" </pre>
CDS	256690..257259	<pre> /gene="gloA" /locus-tag="Psysc-0218" /EC-number="4.4.1.5" /function="Pyruvate metabolism, Lactate biosynthesis" /codon-start=1 /transl-table=11 /product="probable </pre>

		lactoylglutathione lyase"
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gene	complement(257347..2583 57)	/gene="hemF"
		/locus-tag="Psysc-0219"
CDS	complement(257347..2583 57)	/gene="hemF"
		/locus-tag="Psysc-0219"
		/EC-number="1.3.3.3"
		/function="Synthesis of heme"
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		/transl-table=11
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		/protein-id="AAZ18092.1"
		/db-xref="GI:71037784"
		/translation="MSIPNIDNDIKVSSDATTI PSHHDIMRVREFLVDLQARICQAL EAQERDGCADAHKAATFFPDDWERPEGGGRSCV LADGEVIEKAGVMFSHIHVQNLPFA SATARHPDIAGRKAQAMGVSLVVPKPNVPTSH ANVRLFI AEAEKGDP IWWFGGGEF LTPFYVPLADCIHWHQVCHDLCAFPDITVYPDFK QWCDEYFHLRHRDEQRGIGGLFYD DVNTESRGWDFTCFKFMQAVGNGYLEGILPIFE QRKNAPYTEAQREFQLYRRGRVYE YNLVYDRGTLFLGLQSGNGRIESILVSMPPPLASWHY RFEPIEGTPEFELTDFYLPKPRDWL IL"
gene	complement(258376..2590 68)	/gene="ribA"
		/locus-tag="Psysc-0220"
CDS	complement(258376..2590 68)	/gene="ribA"
		/locus-tag="Psysc-0220"
		/EC-number="3.5.4.25"
		/function="Riboflavin synthesis"
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		/transl-table=11
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gene	259652..261694	/gene="dxs"
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CDS	259652..261694	/gene="dxs"
		/locus-tag="Psysc-0221"
		/EC-number="2.2.1.7"
		/function="Catalyzes the thiamine pyrophosphate-dependent acyloin condensation reaction between carbon atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D- xylulose-5-phosphate; synthesis isopentenyl diphosphate"
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CDS       262183..263010

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CDS       complement(263057..2644
84)

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GRLLDRAMPLWECHVIEGIPETEGSPERFALFY
KIHHSVLVDGIAAMRLVKKSLSQSP
NEPVTLP IWSLMAHHRNQIDAIFPKERSALRILK
EQVSTIKPVFTELLNNFKNYNDSS
YVSFTDAPRSILNRRISASRRITAAQSYDIKRFND

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gene complement (264531..2653
55) /gene="thiG"

CDS complement (264531..2653
55) /locus-tag="Psysc-0224"
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/locus-tag="Psysc-0224"
/function="Biosynthesis of
thiamine"
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/transl-table=11
/product="putative thiazole
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/db-xref="GI:71037789"
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LARELLGGHNLVKLEVLGDEKTLYPNVMETLKAA
KVLIDDGFEVMVYTSDDPIVAQEL
ESMGCVAIMPLGSLIGSGLGLINRHTLSLIIENT
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gene complement (265553..2662
87) /locus-tag="Psysc-0225"

CDS complement (265553..2662
87) /locus-tag="Psysc-0225"
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WAWIPKSELEARRQGKANEKSAEV
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gene 266672..268168 /locus-tag="Psysc-0226"

CDS 266672..268168 /locus-tag="Psysc-0226"
/function="endonuclease activity
for DNA repair"
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/product="probable endonuclease"
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/db-xref="GI:71037791"
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HQAYGYEEFVEGIRPMMMAASNQSN
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HSLAPLDMALRRRRFRINCPSQPE
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gene	268184..269728	QTLGIEAQLGHLFSLVSHLEQLQ
CDS	268184..269728	IVLVEQIIPQLAQAAGGQVATLQYIFKDEQQPMQ
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		SPTQQSCQPNKPLADTDIFQTRHVVQNMLSDLMN
		SDDDKSPHSGKNGFGQSSPLIALPV
		AALPLSDWLITQFLQRLAHQHPIITHYQTIHNQT
		ALQGRLLIKEQLRHNSMQPHKFCV
		ERSVLSKGMLANRIIKSALKLLAPLLSQSNLLLY
		LQPVQQVSVLHQYEIRQLASIFYQ
		AKHELAIQPLQAQQLQAQQLVDFAYWLLCQSHA
		ETGHSIDSQNPFFHKLLTPQRLCLL
		IDMNAFEQWASORIALFFQQLSDDYKPLFQTQR
		VWLNDAEGQAQLSIRPDLLIYKQI
		HSSAENTAMYDNYVSQAQDAREKHSRHYSHVIDI
		AYQAQVWLVYPVQDDQORQAVLQKDTQDTYNSE
		NASYAQLWLIPFNVLTAINTDLL PTQDVV"
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tRNA	269965..270041	/locus-tag="Psync-R0007"
		/product="tRNA-Pro"
gene	270136..270212	/locus-tag="Psync-R0008"
tRNA	270136..270212	/locus-tag="Psync-R0008"
		/product="tRNA-Arg"
gene	270252..270327	/locus-tag="Psync-R0009"
tRNA	270252..270327	/locus-tag="Psync-R0009"
		/product="tRNA-His"
gene	270938..272026	/locus-tag="Psync-0228"
CDS	270938..272026	/locus-tag="Psync-0228"
		/codon-start=1
		/transl-table=11
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		/db-xref="GI:71037793"
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		TLKTQFAEYQQYLLAQQLDKRGLM
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		QLTTQDGHNPCLCFATVGKLLKHKP
		IFDQGSLSNYVLGHFGVSSFTYDRGGYIGHVVG
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		DKKLQQQHLVDVLLQLGLMPDINDSTPLF"
		/locus-tag="Psync-0229"
		/pseudo
gene	272937..273497	/locus-tag="Psync-0229"
CDS	272937..273497	/note="thiol:disulfide interchange
		protein; Signal predicted by
		SignalP 2.0 HMM (Signal peptide
		probability 1.000) with cleavage
		site probability 0.555 at residue
		42"
		/pseudo
		/codon-start=1
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gene	273557..275746	/locus-tag="Psc-0230"
CDS	273557..275746	/pseudo /locus-tag="Psc-0230" /note="thiol-disulfide interchange protein; Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.999) with cleavage site probability 0.648 at residue 61"
gene	276220..277656	/pseudo /codon-start=1 /transl-table=11 /gene="pldA"
CDS	276220..277656	/locus-tag="Psc-0231" /gene="pldA" /locus-tag="Psc-0231" /EC-number="3.1.1.32" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.980 at residue 48"
		/codon-start=1 /transl-table=11 /product="probable outer membrane phospholipase A"
		/protein-id="AAZ18102.1" /db-xref="GI:71037794"
		/translation="MFSNITSQRPSLSHSHKAPKK MTLQTNKCSLHIAVGVALTCFTVQ AQAAATAQTYNELPQTKSSQPISTNIAVQNGSL SEEFVAQQAALFFECTQVQTSSAR LACFDKVAEQGKTPSYVTSKQVPDLAKTVISTLS GNPQIILAEETSTITANGNVIAKK VSSNYPODIETKPPAETERLDTVGLTQKEAEVLE SVGVTQADIEKYTPLSLAYDLKDN SERGTWNRPHNPNYVLPFYTADPNLSPNTPSQ DQEQANFTSNNVRQAEKLFQSLK SKVAEDLFDTNADLWFGYTQSHWQVYNEDNSRP FRATDYQPEVFLTQPVIANLPFGG RLRMLGVGAVHSHNGRSEPLSRSNWRIYLMGGAE WGKFSIVPRVWARVDGSSNDNDP DIEDFMSYGDIKFLYDLFNPQSLSGTLRYHPGTN KGSQAQIDYVYPLTKSVNGYVQLFQ GYGESLIDYNYENTAVGVGIVLNDWKGK"
gene	277687..278529	/gene="comF"
CDS	277687..278529	/locus-tag="Psc-0232" /gene="comF" /locus-tag="Psc-0232" /function="natural transformation with exogenous DNA"
		/codon-start=1 /transl-table=11 /product="possible competence protein F"
		/protein-id="AAZ18103.1" /db-xref="GI:71037795"
		/translation="MPALASYQSGWLWLAEYLSIR CQLCRVYRSTPQQLQLNLSLNH SLFSQNSLLAENTSHSLNNHSHFFTNIRKQFHRS CSSGLLCTSCHSSISWLPFPQVD IAADTTLPIQAATYDYPMRQAIRAFKHEDMTK LPLLLHALRQLPRPHGCHQDQNSVI VAMPTTDERLIKRGFDVPSILAAHLSKHWDIPLW QGKIRIDNTLSQQLTRAERLSNL NNAFILIPESPVKRLILFDDVATTGASLQALART LSIYPATTHNANNKCHLYAYVLAH GSQS"
gene	278992..279450	/gene="fimT"
CDS	278992..279450	/locus-tag="Psc-0233" /gene="fimT" /locus-tag="Psc-0233" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability

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0.751) with cleavage site
probability 0.319 at residue 26"
/codon-start=1
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CDS 279450..280100
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/db-xref="GI:71037798"
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CDS 281921..285676
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/Note="Signal predicted by SignalP

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2.0 HMM (Signal peptide probability 0.999) with cleavage site probability 0.426 at residue 35"
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gene 285723..286310
CDS 285723..286310

gene 286310..286747

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gene	287641..288054	/locus-tag="Psyc-0241"
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gene	288187..289947	/locus-tag="Psyc-0242"
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gene complement(290109..290645) /locus-tag="Psync-0243"

CDS complement(290109..290645) /locus-tag="Psync-0243"

/note="Possible transposase and inactivated derivatives (COG1943)."

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gene complement(290794..290919) /locus-tag="Psync-0244"

CDS complement(290794..290919) /locus-tag="Psync-0244"

/pseudo

/note="C-terminus of ferredoxin"

/pseudo

/codon-start=1

/transl-table=11

gene complement(290940..291641) /locus-tag="Psync-0245"

CDS complement(290940..291641) /locus-tag="Psync-0245"

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gene complement(291832..292155) /locus-tag="Psync-0246"

CDS complement(291832..292155) /locus-tag="Psync-0246"

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gene complement(292249..295425) /gene="mutS"

CDS complement(292249..295425) /locus-tag="Psync-0247"

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/function="This family of proteins"

is named after the Salmonella typhimurium MutS protein that is involved in replication repair and plays a role in preventing recombination between non-identical sequences."
 /note="Mismatch repair contributes to the overall fidelity of DNA replication MEDLINE:87297443. It involves the correction of mismatched base pairs that have been missed by the proofreading element of the DNA polymerase complex.; Citation: Tachiki H, Kato R, Masui R, Hasegawa K, Itakura H, Fukuyama K, Kuramitsu S. 1998. Domain organization and functional analysis of Thermus thermophilus MutS protein [erratum: 1998, 26(20):following 4789]. Nucleic Acids Res 26:4153-4159."
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 RREVVKTLTAGTITDDALIAFNHTPTVVAIDILI
 PKNSKQSLQAAISQMDLAAGTLT
 TQTL SANHHDDIEGLKTQMLTVLARFAPSECIIGE
 ALNDSIGGIGEDWLLWLRQSLDCP
 LIEVAANDFHROHASATLCQQFGVQRDLGLGSGI
 SDAPLAQSSCAALIHARQTTQRRQ
 VPQINQLIVEYSDDYLIIDANSQQNLELFTPVSS
 NGTSLLSVLNHCQTIPMGRLLLVQ
 MKRELQHSRINRLDLAIACLLTKDTSIESNQ
 SNQALKHSSLVISREMLNSIGDI
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gene 295988..298777

CDS 295988..298777

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ERRIGDIDDNQITIEVEVELEAERA
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MFAQEVADEKGYTREQMDDEFAIESLSRALTAIKD
NHFKNEIEPVTFKTRKGEQTVDTD
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CDS complement(303315..3046 /gene="hom"
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32)      /gene="dsbC"

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32)      /gene="dsbC"

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bond formation in some periplasmic
proteins."
/note="Citation: Proc Natl Acad
Sci U S A. 1992 Jul
1;89(13):6210-4.
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CDS      306144..307067

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CDS      complement(307312..3115
29)      /locus-tag="Psyc-0256"

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CDS	312743..313759

gene	313900..314607	IAEQPVSLIEAKPLTGRTHQIRVH LAHIGHAILGDNKYHVHDKSGVHRCLLHAWRLDI PGYDTITAPLPDEMLDWMPEEIKS QLPK"
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gene	complement(314697..315605)	/locus-tag="Psyc-0259"
CDS	complement(314697..315605)	/locus-tag="Psyc-0259" /note="GTP-binding domain" /codon-start=1 /transl-table=11 /product="cell division checkpoint GTPase YihA" /protein-id="AAZ18129.1" /db-xref="GI:71037821" /translation="MKDWLLVSSQRGCAIDRAN ANFLLLYLNFKYLNFNRESFMST PFNDVAAQHADFNTKARQRIQQTFFMMSAPTFR CPADIGLEVAFAGRSNAGKSSAIN ALTNQRLARSSKTPGRTOMINFFNVGDADRRV DLFGYGYAAVPLEMKKEWQVELEE YLVSRSSLAGLVMTDIRHFLKFFDEQMLRWAKD GELPVHILLTKADKLKYGASKNAL LNTKRRLKQLGLNCSIQFSAKRKEGLDELAVGM GNWYEQLEANKIIESSFALLEGS ELEDAIEKDAVQKDKNLKDSAQRESK"
gene	315892..316227	/gene="scyA"
CDS	315892..316227	/locus-tag="Psyc-0260" /gene="scyA" /locus-tag="Psyc-0260" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.911 at residue 35" /codon-start=1 /transl-table=11 /product="probable cytochrome c, class I" /protein-id="AAZ18130.1" /db-xref="GI:71037822" /translation="MLSMITMIFAKSNRFLVSSVS AVIISAAMITGAEAANIATTYNES CAACHDSGALNAIKKGDVSVKQOLIKQKGM SSVKNQMIQMPAGGLCEACSNDDY RKLIEYMSK"
gene	316570..317238	/gene="cc4"
CDS	316570..317238	/locus-tag="Psyc-0261" /gene="cc4" /locus-tag="Psyc-0261" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.999 at residue 20"

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gene	317468..318610	
CDS	317468..318610	
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CDS	complement(319028..319444)	

		LRKIVITSILGVAVTMSGCSLLSV YKIDLPQGTPIITQQAQKLQVGMNQNVLYILGS PAIRDTLEPNRWYIYDYQAGTEA RRRGIADVKNASQHLKVYFDNNGIVTGIQGLESL PK" /gene="fur" /locus-tag="Psc-0265" /gene="fur" /locus-tag="Psc-0265" /function="The Ferric uptake regulator or FUR family includes metal ion uptake regulator proteins, which bind to the operator DNA and control the transcription of metal ion-responsive genes." /codon-start=1 /transl-table=11 /product="ferric-uptake regulator family" /protein-id="AAZ18135.1" /db-xref="GI:71037827" /translation="MAGFTNQDLRRAGLKVILPR IKILELLESAAELHHMSAEVYKAL IEQGEDVGLATVYRVLTQFEQAGIVERHNFENN SVFEITQEEHHDHLVCDNCKGIVE FHNKVIIEEQLKVAEAGHGFKLSGHSVLVYGICND QACKDSVK" /gene="pilU"
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CDS	319768..320202	
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gene	complement(320393..3215 14)	
CDS	complement(320393..3215 14)	
		/locus-tag="Psc-0267" /gene="piliT" /locus-tag="Psc-0267" /function="Pilus retraction protein: required for twitching motility and social gliding. Protein involved in type II secretion." /codon-start=1 /transl-table=11 /product="pilus retraction protein PilT" /protein-id="AAZ18137.1" /db-xref="GI:71037829" /translation="MAEQNLRIEDLLRFVAVKLKA
gene	complement(321690..3227 42)	
CDS	complement(321690..3227 42)	

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gene	323058..323813	
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		/note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.996) with cleavage site probability 0.413 at residue 29" /locus-tag="Psc-0269"
gene	complement(324062..3253 36)	
CDS	complement(324062..3253 36)	
		/note="Transporter associated domain and two CBS domains present. RBS found. Signal peptide and 4 transmembrane helices predicted." /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="AAZ18139.1" /db-xref="GI:71037831" /translation="MSLLTAGVFIFILIALSAIV SSELALASARKIKLQVMAKEGEV RALDVLNMQEQPGSFITVVQVALNAVAILAGVIG ESAVSPYLQRLFGNETAASVVSFI LVTSMEVLFADLMPKRLAMSNAEPIAVKMRPMI FFIIFIKPIIWWFDGAANLLFKLI GVSTVRQDEMTSIEDIYAVMDAGAEAGVIKHQEH LIENIFEMQERTVTSVMNPREHIV YFDTKASTEQQVAVMIKQPHNKFVLCNDDLEHI IGYVESRSFLASVLEQQVECLTDK ALLKPAFLIPDTLSLFEVLETFKSTGADFAVIVN EYALVVGVIITLKDVMISVMGELVT LEEQPIVQRTDNSWLIDGMTPIEDVIRSLGMVNL PHSQNYETISGFMYYMLRKIPKKT DCVEYANYRFEIATDNLKITQLLVTKFEDVI" /gene="nadE" /locus-tag="Psc-0270" /gene="nadE" /locus-tag="Psc-0270" /EC-number="6.3.5.1" /function="NAD synthesis" /codon-start=1
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CDS 346048..348033

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CDS complement(348127..348966)

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gene complement(349170..349796)
CDS complement(349170..349796)

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CDS	complement(358637..359938)
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CDS	374402..375073	
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 proteins involved in cell cycle
 checkpoint functions responsive to
 DNA damage).; Citation: Lee JY,
 Chang C, Song HK, Moon J, Yang JK,
 Kim HK, Kwon ST, Suh SW. 2000.
 Crystal structure of
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 19:1119-1129."
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gene      complement(404366..4048
42)
CDS       complement(404366..4048
42)

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ribosomes such as occur during
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lacks a stop codon."
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 Serine peptidase. MEROPS family
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CDS	409080..410876
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TNLNVVLVINKADTLKDKGSVLPL
METFNDSFDFADIVPVSALKQNLDRLQEVIAH
LPVAAPYDTEQITDRSERFLASE
IIREKIMRSAGDEVYPDLTVQIDGFKDEAAHTDP
KTGRPRKACTFIDATIIYVERSGQK
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CDS 414720..415484
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CDS 415584..416378

gene complement(416416..417003)
CDS complement(416416..417003)

gene 417594..418778
CDS 417594..418778

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ADELRCLRHFE SYLFNELGFSLT
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21)
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glycosylase (Fpg) is a DNA repair
enzyme that excises oxidized
purines from damaged DNA (base
excision repair)."
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/note="Citation: Gilboa R, Zharkov
DO, Golan G, Fernandes AS,
Gerchman SE, Matz E, Kycia JH,
Grollman AP, Shoham G. 2002.
Structure of
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glycosylase covalently complexed
to DNA. J Biol Chem.
277:19811-19816."

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84)                                     /locus-tag="Psc-0346"
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CDS 430705..434112 /locus-tag="Psc-0347"
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                                     GSI LGFEFDQTLWLLVMDSEPLYIARYIAMAL
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gene 434240..435052
CDS 434240..435052

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gene 435269..436528
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pump, Bcr/CflA subfamily"
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gene 436838..437632
CDS 436838..437632

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REALERTDRMEKLESLGGIKDMG
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gene 437862..438746

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gene	complement(438893..439714)	/locus-tag="Psyc-0352" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 1.000) with cleavage site probability 0.462 at residue 32"
CDS	complement(438893..439714)	/locus-tag="Psyc-0352" /function="Bacterial lytic transglycosylases degrade murein via cleavage of the beta-1,4-glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine, with the concomitant formation of a 1,6-anhydrobond in the muramic acid residue." /codon-start=1 /transl-table=11 /product="possible lytic transglycosylase" /protein-id="AAZ18221.1" /db-xref="GI:71037913" /translation="MINIAPFMTIRCLSPILLTAV ALSSLPIAAQAGNMYIYKDKGGQV LLTNVNPSTGNFDFKTKKVKVITYYKSSLYDSGSS NSSNDYGSSSASSSGTRNSYDSYI LASAQRHGVDPGLMKAMMHTESAFNPNARSVPVGA QGLMLQMPATARRFKVSNPNWNPAD NIEGSAKYIAWLMRRFRNNNVFAVAGYNAGEGNI DKYNGIPPPFKETRNYVKSVMRSYH SLYKNDSTGLSGNSMNNNSNIGTTSNGGQIGNVS YGTSSNSNPSYANSAYLALR"
gene	complement(440145..440834)	/locus-tag="Psyc-0353" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.621) with cleavage site probability 0.473 at residue 21"
CDS	complement(440145..440834)	/locus-tag="Psyc-0353" /codon-start=1 /transl-table=11 /product="conserved hypothetical protein" /protein-id="AAZ18222.1" /db-xref="GI:71037914" /translation="MSFDNVFVATLAAILLTLTA HIIARILARKLSWLPMTVITALVLV VILLIFRWDYNYHYGVAKPVDFHLLGYVTVLLA IPLAAMNFKGLPVKKLVLIVAMAS LIGALLPMSLAYLFLSLSHDTIILAFASRSVTTPIG

LSIADLIKAPLANLIIVSGII
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 gene complement(440866..4412 /locus-tag="Psc-0354"
 94)
 /note="Signal predicted by SignalP
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 probability 0.409 at residue 29"
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 CDS complement(441586..4430 /gene="hflX"
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gene complement(444568..445608) /locus-tag="Psyc-0357"

CDS complement(444568..445608) /locus-tag="Psyc-0357"

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gene complement(445651..446148) /locus-tag="Psyc-0358"

CDS complement(445651..446148) /locus-tag="Psyc-0358"

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/protein-id="AAZ18227.1"
/db-xref="GI:71037919"
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gene 446465..447346 /locus-tag="Psyc-0359"

CDS 446465..447346 /locus-tag="Psyc-0359"

/function="Autonomous mobile genetic elements such as transposon or insertion sequences (IS) encode an enzyme, transposase, that is required for excising and inserting the mobile element."
/note="There are 9 additional ORFs identical to this one."
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CDS 448233..449150 /locus-tag="Psyc-0360"
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 QKAAEQGHASQFNLGSLYRDGKGVQDDFSLAAE
 WYQKAAEQGHASQFNLGSLYQDG
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 EGKDVQDDFALAAKWKYQKAAEQGH
 IASQFNLGSLYQEGKDVQDDFALAAKWKYQKAAEQ
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 26)
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 DIDLQQRGLGSLYQVEYAEFFQAHAA DD"
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 CDS complement(450659..4511 /locus-tag="Psyc-0363"
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 Aspartic peptidase. MEROPS family
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 gene complement(451302..4541 /gene="ileS"
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 CDS complement(451302..4541 /locus-tag="Psyc-0364"
 27) /gene="ileS"

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gene      complement(455427..4570
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64)      /locus-tag="Psysc-0366"

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activity:adenine deaminase that
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hypoxanthine and ammonia which is
important for adenine utilization
as a purine and also as a nitrogen
source"

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CDS	457612..458244	
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gene	460224..461450	
CDS	460224..461450	

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SLEELLSTADIVTLHVPELPSTRY
MMKAEQFAHMKEGSYFINAARGTCVEIDDLTAVL
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FVRYSDQGNATATAVNFPEVSIPIK
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AMFCTGGIRCEKSAFMREQGFEE
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gene complement(464315..4648
96) /locus-tag="Psync-0373"
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1.000) with cleavage site
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CDS complement(465913..4672
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 QSILSDPDFKNGRYLQAGTYPRRG
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 EKLMSFSGHIGIPQPYADKGDYPYKR
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 /locus-tag="Psysc-0378"
 /EC-number="2.7.7.7"
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 polymerases are the key enzymes
 catalyzing the accurate
 replication of DNA. They require
 either a small RNA molecule or a
 protein as a primer for the de
 novo synthesis of a DNA chain.
 This protein also contains 5'-3'
 exonuclease domains."
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CDS       complement(472843..4732 /locus-tag="Psc-0379"
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          SADEFQQLVEKANKVCPYSKAIHGNVDSEVISEV
          K"
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          RTLTAVDSALMMVDGAGKVEERTIKLMEVCRMMD
          TPIISFVNKLDRQIREPLELLSEI
          EAVLKIKCIPITWPIGMQDFGVYHLTENKTYF
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 /locus-tag="Psyc-0382"
 /note="Forkhead-associated (FHA)
 domain. The domain is present in
 a diverse range of proteins, such
 as kinases, phosphatases,
 kinesins, transcription factors,
 RNA-binding proteins and metabolic
 enzymes which partake in many
 different cellular processes"
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 protein"
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 EPVINKATVSEITFSETSYASEAFV
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CDS	476550..476816
gene	476897..477853
CDS	476897..477853
gene	478244..478319
tRNA	478244..478319
gene	478385..478468
tRNA	478385..478468
gene	478555..478628
tRNA	478555..478628
gene	478733..478807
tRNA	478733..478807
gene	479294..480484
CDS	479294..480484

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IAMDKGLRFAIREGGRTVGAGVVA NVHV"
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CDS       complement(481988..4824 /locus-tag="Psync-0386"
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gene      complement(482733..4835 /locus-tag="Psync-0387"
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CDS       complement(482733..4835 /locus-tag="Psync-0387"
39)
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transferase"
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gene      complement(483610..4846
32)

CDS       complement(483610..4846
32)

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gene      485598..488804

CDS       485598..488804

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block in cell division and it is
involved in peptidoglycan
synthesis or modification."
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gene complement(489143..4896 /locus-tag="Psyc-0390"
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CDS complement(489143..4896 /locus-tag="Psyc-0390"
 31)

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gene complement(489872..4904 /gene="dnaQ"
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 polymerase III core enzyme
 (responsible for chromosome
 replication)."
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 III, epsilon subunit"
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 LANLGYPLCEGNIMMTPMWRQPL
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 QFARAALQFGDINQWQKLVPPLGGKPISYITDL
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EYFLREIAEDILWHEALNLHHPFIGRASNADSPF
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CDS       complement(497967..4987
61)

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CDS       499186..499533
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CDS	500233..500403	/locus-tag="Psync-0401" /note="Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.839) with cleavage site probability 0.547 at residue 22" /gene="dcm" /locus-tag="Psync-0401" /function="C-5 cytosine-specific DNA methylases specifically methylate the C-5 carbon of cytosines in DNA to produce C5-methylcytosine. In bacteria, these enzymes are a component of restriction-modification systems." /note="Citation: Lauster R, Trautner TA, Noyer-Weidner M. 1989. Cytosine-specific type II DNA methyltransferases. A conserved enzyme core with variable target-recognizing domains. J Mol Biol. 206(2):305-12." /codon-start=1 /transl-table=11 /product="probable C-5 cytosine-specific DNA methylase"
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CDS	complement(500671..502233)	

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CDS	complement(503979..5077 94)	/gene="meth"
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		/EC-number="2.1.1.13"
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 with cleavage site probability
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CDS	508533..509117
gene	509429..510031
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CDS	complement(510427..511761)	/pseudo /locus-tag="Psync-0406"
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CDS	511927..512808	/locus-tag="Psync-0407"
		/function="Autonomous mobile genetic elements such as transposon or insertion sequences (IS) encode an enzyme, transposase, that is required for excising and inserting the mobile element."
		/note="There are 9 additional ORFs identical to this one."
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		/db-xref="GI:71037965"
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gene	complement(512800..512964)	/locus-tag="Psync-0408"
CDS	complement(512800..512964)	/pseudo /locus-tag="Psync-0408"
		/note="sodium/alanine symporter"
		/pseudo
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		/transl-table=11
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gene	514839..515999	/locus-tag="Psync-0410"
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CDS	516094..516618	
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gene	517547..517894	
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gene	517955..518836	
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gene complement(551327..5516 /locus-tag="Psc-0441"
50)

CDS complement(551327..5516 /locus-tag="Psc-0441"
50)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18304.1"
/db-xref="GI:71037996"
/translation="MLDKDETTYSLLTYLWVFL
ALTGGLVAFIRRLNRSRKPLPLTE
VFVRLMGELIISGFAGVLTIFYLCEYWGFDQLFTA
VLVAISGHLGGGAIDRIAKIWDA IDKTP"

gene complement(551715..5522 /locus-tag="Psc-0442"
56)

CDS complement(551715..5522 /locus-tag="Psc-0442"
56)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18305.1"
/db-xref="GI:71037997"
/translation="MFFVIYNTETGNITQTVSAP
FYPMPMFVLEEFGAVLEVDPQND
DKEHIKDGVLVAKPEPIIDPKVTKVLEQDKVWDS
IKRRLSQITNGVLVESVKNFTHT
DSMSAIQYSTIAGMAAMGTQTVNWKVMDNSWVL
LTVELLKELQVAISVKTNTNIEVA
EQHKAAMLLVDNPLEYDSTNNW"

gene complement(552271..5554 /locus-tag="Psc-0443"
44)

CDS complement(552271..5554 /locus-tag="Psc-0443"
44)
/codon-start=1
/transl-table=11
/product="putative prophage
LambdaSo, host specificity protein
J"
/protein-id="AAZ18306.1"
/db-xref="GI:71037998"

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/translation="MSDVITIQQAKAGQQASRP
SIADDTIASISRLKMIIGLSEGEV
KGLANGAKSIMLEGTPLEDANGNRNFDGVEWEIR
HGTVDQTYIAGMPNASSEIGVGT
VRSDTPWIRSINDTQLSSINVNISFPMKSVTDK
GDVVGVTVDYAIDVQTDGGGYVPV
ITKSLTAKTSGRYQRTHNVALPEAQSNWQIRIRK
ITTDNGETLFTNTMQIDISIAEIID
GKFNPYHTAHLYSFDDARTFSSIPKVSVDMLGVY
VQVPINYDTRTSTGIWNGQFKL
GYTTPAWHYNYLITNDRYGLGDKLQAFMIDKWA
LEHIAICDEPDDGKGGTEPRFE
CNLYLQKSEDAVQLQHIAGIFRGMMSFWNGSQIF
VDADTSRDCEYVITRANVIGGQFS
KSGSAASDRHTIAQVAWSNPNDTYETEYVMVRNE
RAIAQQGINVLDLSAVGCTSEGA
YRMGLAALLAEQNRITQTVSFAMGLDGSFPNVGSR
IDIAAMMFTGANNGRISSVSADY
TVITVDRDNIQATVGDKLVNLESKAQTRVITA
INGRAITVALAFDPVSAQNVWAIN
SNELPTMPFIVMSVTSDEDTQYNYTAMQYDPTM
YAQIDNGTIEQRPPVPSNNPYII
NAPDAVTLSSRRHVAQAIVTTLEITWSQVKDAV
AYDVEWRKDDGDGDIKLPRTGNSIA
EIDGVYSGNYLARVRVSAFDAISKPTTSMILTAI
TGKAGTPTTVVGLTATGALFGMEL
KWSFDIGSDDTAYTEIEVGSAPATNVTLGQFGY
PTNMTIITGLQNLSSQSYRARIVD
KLGFAWSSWVATNTNNSVSDIFDLITGTEFDT
DSPFIDIPAGTVIGGVAIPEGVYL
RSTFIQDASIDNAKIKNLGDKITANTITASKLA
ANTITADKIATGTITASGVIGDL
AVDTLQIAGNAVTVPLAVYTEASINTSFYSKAFD
IQSIVVPDISARKAVHFNFSYTIK
SAGEVSALSMSFEVKLDGVVIRKGAVASSYNSTR
VYGQCSSLLDDTQFGTLTIIVS
TSGDGGFIPLDSSGVSNRFSVITKR"
gene      complement(555447..5560 /locus-tag="Psync-0444"
10)
CDS        complement(555447..5560 /locus-tag="Psync-0444"
10)
/translation="MLRRIELHGLAEKFGKSFE
LDVASPREACTALGYQIDGFKQFM
MTAHESGLFFAVFNDDENIGANIEHNTGASIIIR
VPEIVGAGGVDVGGWLQVVGAAAL
VAVGVFVPMQWAIAGAGVGLMIGGAASLLMPTPN
IESQDEAGNKASYAFGGAVITVAQ
GNPVPILLGRHEIGGFIISISIVNEDT"
gene      complement(556066..5568 /locus-tag="Psync-0445"
15)
CDS        complement(556066..5568 /locus-tag="Psync-0445"
15)
/translation="MYILKDAKDAMLNHAACYP
HECCGLLVNRQYIECENIADNDSE
FKINPRDVRAEKLGKIEAIVHSHPNGSTKPTSF
DLIQMQHNNVPWIIIVAYPEIDIKV
HAVKDYKAPLINREYIHGVLDCFSIVRDYYSREL
DIQIDNFERQDKWVESVSNADLYV
DNFASQGFVQVDSLQRHVDILCRVQPTHEVNHAI
IYLGDNGLTSEQEKVINDHLVL

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gene complement(556815..5576 /locus-tag="Psync-0446"
33)

CDS complement(556815..5576 /locus-tag="Psync-0446"
33)

/codon-start=1
/transl-table=11
/product="probable phage minor
tail protein"
/protein-id="AAZ18309.1"
/db-xref="GI:71038001"
/translation="MLSSDLQKLSVTGLVTLIEL
DAIKLGGAIFRWHGHVNWEDWRKI
FVWAGSTESLAGDES LAGEDYFAS TTETETIYRN
IIWQGQTYTPIAIQSDGLEVRGDG
RPSAPTLVIANKIDDTLGAIVCAFYNDFVGAT
LTVTHVLAKYLDAAFAVGNPTAN
PSESMQYQWYVEQKTEENEQTVTFELASPLSAQR
KKIPTRNITPYCTWAVRGKYRGES
CRYMGTSMTFEDGTATDDPALDKCGGRLVDCCLR
FGENEPLNFGGFPASQLRGG"

gene complement(557921..5590 /locus-tag="Psync-0447"
09)

CDS complement(557921..5590 /locus-tag="Psync-0447"
09)

/function="Reverse transcriptase
uses an RNA template to produce
DNA, for integration into the host
genome and exploitation of a host
cell (strategy employed in the
replication of retroviral elements,
such as the retroviruses and
bacterial retrons)."
/note="Within putative prophage."
/codon-start=1
/transl-table=11
/product="possible RNA-directed
DNA polymerase (Reverse
transcriptase)"
/protein-id="AAZ18310.1"
/db-xref="GI:71038002"
/translation="MFFLRIVMKRIGNLYESVVS
GESLWEGYLGAKSKGGRRGCFQF
EKS LGRELNELQEELANNITYKPRPYFKFIVYEPK
KREIYAPAFRDCVVQYAIYLRVMP
IFDKTFIDQSFACRIGLGHKAAEYQAQDALRRAG
PNITYTLQLDIKKFFYSIDRPTLRK
LLERKIKDKRLVDLMLMLFADYEPKGP IIGNLLS
QMFAIYMNPDVHDYATRVLKPAAG
YCRYVDDFLFGLTRAQALTYRKLITDFVEQKLR
LTLRSSTIANTRKANFCGYRIWR
SGRFIRKHSYKTRKAVRANKLESVISHLAHASK
THSLQHLNLNAYEQNHGLYQLQPK
IYHTRHHQAVERSGRINGVMNRCSNVN"

gene complement(559269..5596 /locus-tag="Psync-0448"
52)

CDS complement(559269..5596 /locus-tag="Psync-0448"
52)

/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18311.1"
/db-xref="GI:71038003"
/translation="MAVDSSENLDDKKFIQTMKLL
NIYLNHFPSHEKHGLALKIRQTAY
DMYDYIVEAQKRYHKKTTLNLDIKHEQLRMQVR
LAFELSYFGHPKTEKMSVQKLNK
RYLVISASIDEIGKTIIGGWIKSLKQ"

gene complement(559678..5611 /locus-tag="Psync-0449"
44)

CDS complement(559678..5611 /locus-tag="Psync-0449"
44)

		/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18312.1" /db-xref="GI:71038004" /translation="MQIQKINLGAEPSSIGGDSA RTSNGKVNTNFDADVVAEFADVRA5 IPSVTSDLGQSTTIIAISQKLEDTILMSQFNDIGV QGALGFGTIGITNKLPITGMSQMGGI AIKGHENWNGNYQYSDGSVMVIVPRFYRWGHVNS PNYAKYGVNALDVKSIYDFVDVVA ANAAGYALHRAFYDDGQIKDGGFVVDKYQCSNNAG KASSIKNGIPLSSSSANAPFSGLI GAPANTLAGAIDAAKTRGSFAFFATTIFIQRALS LSMAHAQAATSSAACAWYDATGVN NFPFKGNNNNALRDVNDITAVLYEGTGYLTAGTKGS AQPFKTTTHNGQYSGVADLNGNMW EVALGLTQTAGSFYVLRTSAKASALTSGATLATD AWGTAAMTASYDLSGLASYGELTGV VRNFAIGSTTNQVFSSTANSGLAWSASCAGIPQLG GAGGTNAYGNDRFYDNRIEHLCP VGGNWSYGAYAGVWAVHCYFSRTNGDHHFGVRAA LYSV"
gene	complement (561153..561491)	/locus-tag="Psyc-0450"
CDS	complement (561153..561491)	/locus-tag="Psyc-0450"
		/codon-start=1 /transl-table=11 /product="possible LambdaSo, minor tail protein M" /protein-id="AAZ18313.1" /db-xref="GI:71038005" /translation="MIKTFPWQIDMGASADKQYR VKKTQFGDGYTQHSSTGINNTKN WSGTKTGALDTVIKPIEAFIDEHAGVLPFYWTDP HGNTKQYTCAGASIPQRKGDYWQI TINFEEQFNNT"
gene	complement (561553..561825)	/locus-tag="Psyc-0451"
CDS	complement (561553..561825)	/locus-tag="Psyc-0451"
		/note="similar to Shewanella oneidensis hypothetical protein SO2991" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18314.1" /db-xref="GI:71038006" /translation="MVTVTRDSGVLGSACAMKLS IDDNVAALKRPSDAVTLHIPNGRH IISFDTRGGLCPSTDAIDVSLNKGDVKKYRIRA DMNGNFQLLPTL"
gene	complement (562011..565082)	/locus-tag="Psyc-0452"
CDS	complement (562011..565082)	/locus-tag="Psyc-0452"
		/codon-start=1 /transl-table=11 /product="possible pore-forming tail tip protein" /protein-id="AAZ18315.1" /db-xref="GI:71038007" /translation="MAVLSYLEIVLAANSAAFNQ SIADARTQTVAAFSDMREYANKMG PAVGAAIGVAAAATTALVVEQVALANELQHTANV ANSSVQEIQKYITVGAKMGIEQDA LGAIFQDTSKIDGFLSTGGGGMADFFENIAPQI GVTDAEFRNLSGPQALQLYYDSLE KAKIGQNEMTFYMEAMASDATTLIPLLANGGEF DYWAKAANAGAVMDDETIVATOK

LQATTDLLELSVDGAKTQFVKGFIPVLADVATKL
 TGTETASDAAYLAGONLAIGFKGV
 AKVGVGAATFDVAGSSIGGVAIISTLLDGVGI
 ADSGLEIAIKMGSNIIKAAGEMNRM
 VDDIRDLSYADLLKGVDELGGSGISNATVDAL
 IEQKKRLAEINQELGKTGQEQEQEQ
 QEAAKKAAEDKAKADKAAKAAKELGAAYVSNTA
 LSGLLKLANEATAGKVRGYTAEF
 AEVTQSLGNDLKYFSALNDTYHKGTNSKHASGQ
 AFDVVLKNANQAASAAAI IKKAAA
 QYGYSVKVLNEYANPSKNATGGHLHVSVYGKAT
 KAGGADIQYIKQNNALAQEQQRA
 ASEQARILEQQSKDRTAIRMEYANAATRIEMQLA
 NQIDKINASGFNDERTAFIDDAI
 DVANTKLAQMLTHDQEQYAAQSQEQTDAERIRN
 QYALERREIQLTIKMDKELRKAKI
 DALNQAEQLALDERRYAFSELRQLTSIGQSDLA
 ALRQSYADQRRALDMRTDINPSQK
 SDLRNAMAGAQIYDTGLOKQKARDGFNAQQADMN
 GTGANYSIAQQYKSRLDVIAKAAE
 AELNLTVSYYQAKLDAQREFVMAATQTLTSTAEQ
 TAASLAGSFKTMLGEONLAYKLMF
 AGQQSVFMAAGLNNYEAAGDAMAEATLSQKIA
 GAATIATEFARIISAASSMTLELP
 GYQTGGFTATGRDSDPAGLVHANEFVANAPITRK
 YRPELEAMHNGTYDRQSSAFNINV
 NVTYSMDGNSNVENSQYKQIGQLAAVVSSEV
 MKMMRPNGTLDKTYAKR"

gene complement(565254..5657 /locus-tag="Psc-0453"
 84)
 CDS complement(565254..5657 /locus-tag="Psc-0453"
 84)
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAZ18316.1"
 /db-xref="GI:71038008"
 /translation="MANLIQCKDCGNQISKNAKS
 CPNCGAENKQTSIITWLALIFIGI
 FVLHVSFVSGAANDIFSEPVAEVEEVSLETLETF
 DLDQDNFDKRAWAAASYSQMLIKQ
 SMKDPASAEFGSIRYKASKEFFATICSQVNGKN
 SFNAYSQFKDYILPELGIYNIDD
 GTVEFKKANDFCILK"

gene complement(565850..5660 /locus-tag="Psc-0454"
 74)
 CDS complement(565850..5660 /locus-tag="Psc-0454"
 74)
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAZ18317.1"
 /db-xref="GI:71038009"
 /translation="MAYYNIDPWGGYRSIDIQTAQ
 IEAGITSYTGSLYDILSFNPNPLP
 AEQIEKRAKAAQIAKLERETQMAKMFDA"

gene complement(566176..5665 /locus-tag="Psc-0455"
 41)
 CDS complement(566176..5665 /locus-tag="Psc-0455"
 41)
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAZ18318.1"
 /db-xref="GI:71038010"
 /translation="MSKQLTAALIAACIAELPTG
 HISMPHKLGGNVNIIKHNVARE
 AFEKAAFGADSEFKDYPQRAVTFAHAVVDENGKR
 LFGDDQIPVISEWPAYVTMPVFOR
 YNEINGVGPDKVEAEKNS"

gene complement(566615..5670 /locus-tag="Psc-0456"
 37)

CDS complement(566615..5670 /locus-tag="Psc-0456"
37)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18319.1"
/db-xref="GI:71038011"
/translation="MAKENIVDSFYRLNMDLIGD
GLTFTKIPLLQECAPPAEKTSDT
ITATDDQEEVTVVVDFKKNQSIDFEVVYDPTDPT
HMLADAMWATNGYKDFEYEFVKLA
RKKITTAQLMKWEESTDKEKKLRMKGSLTISNLI
TTTV"

gene complement(567059..5674 /locus-tag="Psc-0457"
18)

CDS complement(567059..5674 /locus-tag="Psc-0457"
18)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18320.1"
/db-xref="GI:71038012"
/translation="MDASKLIKSVLDPIVAGRVY
PLKVPETAATAAIVKGKPYIVYTPIT
SIDITDDGHTGHERVPIQIDVYATTYGEANDTM
KLALKQISNNIEGAADFGRSPFFD
PDLYRQTADIRIWGTIF"

gene complement(567436..5679 /locus-tag="Psc-0458"
03)

CDS complement(567436..5679 /locus-tag="Psc-0458"
03)
/note="Part of a putative
prophage"
/codon-start=1
/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAZ18321.1"
/db-xref="GI:71038013"
/translation="MSNDLMNIEFEVLGLSELDN
ALAEITLSMQKKTLEGAALMKALP
IMKAANKNANKSEAAHQKLYNDGQFTTIQPGTLK
KSIQRQRMKSKLFSVTVRVKKSR
GKPYPIYWHFVERGNSRMVATPYLRPAFEQNVEL
AIQLFSEELTKRIDKLTQD"

gene complement(567896..5682 /locus-tag="Psc-0459"
28)

CDS complement(567896..5682 /locus-tag="Psc-0459"
28)
/codon-start=1
/transl-table=11
/product="possible phage head-tail
adaptor protein"
/protein-id="AAZ18322.1"
/db-xref="GI:71038014"
/translation="MAKISGRGLSTPIGILRATA
TEDDYGDITISSFGEVSQTFCEWLP
LSANAVIQAHTEGMTISAKLHVDLNTDINQTDKI
KNLADNQVYEVITVMPVPADNKKI IICKVSNV"

gene complement(568230..5685 /locus-tag="Psc-0460"
38)

CDS complement(568230..5685 /locus-tag="Psc-0460"
38)
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18323.1"
/db-xref="GI:71038015"
/translation="MITSSITLDQAKSHLRVMT
IDDAYIAGLIPTAHLIADEIDRE
LTEDICLTPTIGELSESRLHAALLVIGDLYQNREA
QQTEQLHMNHALERLLNKYRKMGV"

gene complement(568652..5699 /locus-tag="Psync-0461"
05)
/note="Signal predicted by SignalP
2.0 HMM (Signal peptide probability
0.922) with cleavage site
probability 0.637 at residue 24"

CDS complement(568652..5699 /locus-tag="Psync-0461"
05)
/codon-start=1
/transl-table=11
/product="possible major phage
capsid subunit precursor"
/protein-id="AAZ18324.1"
/db-xref="GI:71038016"
/translation="MRDIKKTALVCAIASMGVVT
RDAGGSKDEYEKLAGQLKTRLTTL
DKLIEDKQKLLTDDKADTESRNAAIKDLQDSVKD
VGELSARFEELEQKMVRGVQDGD
DPNSIGGILLSRNEGISQEIKAIKHSRGKVQIDGV
SARNTVLLGTINTAGNINDAKMVA
ATEDPLTIVTMINWIPITAPLIPYVRESAVIFMA
DIVPEGMLKPESSLTFGVDSLEID
VIAHWIQVSNQVLLDDAPALAAAYIEGRMAYGVRLK
LEYLVINGDTKSFKGLMKVGNLSLT
IVSNDNAIDTISTAKAKAYANLPPETVILNPQD
WAGIEQVKGTGDGHYIFGSPGAAYVQ
PVLWGLKVMQSPAMAIGKFAGNITMATEGYIRQ
DVTVELSTEDSDNFRKNLVITRAE
MRAAFGVVMPDAAVTGDVLNVVGPVV"

gene complement(569983..5707 /locus-tag="Psync-0462"
29)

CDS complement(569983..5707 /locus-tag="Psync-0462"
29)
/codon-start=1
/transl-table=11
/product="prohead peptidase.
Unknown type peptidase. MEROPS
family U35"
/protein-id="AAZ18325.1"
/db-xref="GI:71038017"
/translation="MNKHSLQTMRCRDRSELLQ
SVSTRMPLIIDTKIRFAEPKGDGA
ATYTFEGYAVKWDSINLHGEKFARGAFSDMITAF
ENDAKTVHMYYNHGWNRNMFNLNAA
MRVGRWVEFEEDDGLRVKGELTQGLPLATAVGA
MMRHLITVDGLSICFYNPTEM DYEE
QEGHILIKRADLFEISVDEPSPDRSARVNRQSET
INNLAERDADCMLETKGLDQADA
RHFITKLDLSIMGTSADDTISKNDPFAFLDS"

gene complement(570722..5719 /locus-tag="Psync-0463"
57)

CDS complement(570722..5719 /locus-tag="Psync-0463"
57)
/function="it forms the junction
between the phage head (capsid)
and the tail proteins"
/codon-start=1
/transl-table=11
/product="probable phage portal
protein"
/protein-id="AAZ18326.1"
/db-xref="GI:71038018"
/translation="MAIIQSVAAWFGYAPRPDVPD
GNQNAVRTVTKTAKPVTFDASMTV
TAVFASIRLLAETIASMPIEMYTKDKDGTLDLAKA
DHDLIKLLRYKPNKRQNRNIEFMEQ
LMLNLVSDGNAYVRITRIGEKNSRIISLDIINSS
NMTVILKNDELIRHQITSAFSRD
FKESDIWHVKLFGNGIKGLSPLQHATKAVAVADA
SDDKITSLMRNGAKPTGALMTKGN
PTAEQRTALRNEMASLTSGDETTFMPVLPLDMKFE
AISLTPSDIELLATRRFSLEEIAR

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MFGVPSILINDSTQSTNWGSGIASIIEAFHKFNL
RPLYERLELSMLTSLVPRKDWDRY
QFEIDADAILRSSRKERVAMYNTISTGQRTPNP
IRRAEGWKPKQEGGDNLYMQLGFAF
LSVVAKQPPPNQTKDTSNE"
gene      complement(571959..5737 /locus-tag="Psyc-0464"
04)
CDS      complement(571959..5737 /locus-tag="Psyc-0464"
04)

/function="Terminases cleave the
cohesive ends of lambda family
phage."
/note="Often located next to the
small subunit."
/codon-start=1
/transl-table=11
/product="probable phage
terminase, large subunit"
/protein-id="AAZ18327.1"
/db-xref="GI:71038019"
/translation="MSDVIAYANIATQYATDVVD
GTTDACVYVRQACQORHLTDLDRAK
NESAFEFEFNSQLAAKACRFIELLPHVKGELANR
RELILLEPWQIFIIANLFGWVDFD
GKRRFRYAYVEVPRKNKSTLAAGIGLYLGFADG
EMGAEVYSAAATTIDQARIVFETAQ
SMVRKRFPDMQKAMGIEVSAHAVSSIATASTFKAV
SRDYGGNLDGLNVQGALIDELHAH
KSNDTYEVMATGMGAREQPLFAITTAGFILDGV
CYEORTLVTKVLGSLGSHDRYFGI
IYITIDEADDWRDPQSWRKANPNYGISVHKDALQA
EYQRAAISPDQAQDFLTKHLCVWV
AARSGWLNMQDWDADAADKTLVAGLFDKYPCFGL
DLASKVDLAARIKLFVKKIDDESH
YYLFANFYINRAQLDNANNANQKRFIEWERQGWL
TVTDGNITDFEKIERDIIHDSQY
DMQETGYDPFNATYLAMLRNEQGLNMVEVPQRVA
YLSPEMKHLQALLTSKRVHHDGNP
ILRWCMGNVTVKKDANDNVFPRKESDANKIDGAV
AAIIATNRAQYYDETGDLPSKDFE
SQLGDYLTDFVSFRG"
gene      complement(573711..5741 /locus-tag="Psyc-0465"
84)
CDS      complement(573711..5741 /locus-tag="Psyc-0465"
84)

/function="Terminases cleave the
cohesive ends of lambda family
phage."
/note="Members tend to be adjacent
to the phage terminase large
subunit gene."
/codon-start=1
/transl-table=11
/product="possible phage
terminase, small subunit"
/protein-id="AAZ18328.1"
/db-xref="GI:71038020"
/translation="MARPRKPTQLKVLQGSRRVS
DREAAASNAQPTIAVPPCPDWLDA
KSRKQWDKIAPQLVALGLLSVIDGDLFGAYAETS
ARYGDVCSKLENIKDWIGTTPNGF
EVQTLVSIIRNTLQKQLISLGREFGLSPAARSSI
KVDVSPQGLFGDDEFKDFKQG"
gene      complement(574289..5747 /locus-tag="Psyc-0466"
35)
CDS      complement(574289..5747 /locus-tag="Psyc-0466"
35)

/codon-start=1
/transl-table=11
/product="possible phage holin
protein"
/protein-id="AAZ18329.1"

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/db-xref="GI:71038021"
/translation="MPLMPTTLCSHAGCNARAVG
NGVCRIHKPKAKRQAPNQIKQAEK
AKLKRIDHRLSASQRGYDVRWSARLLFLNDEPL
CRHCITQDITKGADVVDHILPHRG
NQELFWDQTNWQPLCYCHSIKTTTVDNKLSDYD
IAQLRQGGWGKK"
gene      complement(574862..5752 /locus-tag="Psc-0467"
63)
CDS       complement(574862..5752 /locus-tag="Psc-0467"
63)

/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18330.1"
/db-xref="GI:71038022"
/translation="MRQEYLRAAAEAYANLSDLG
SDCYHYLNDGFPEVQPRLVATYAT
ALLTTEIPSKYINKIVRTALVEWQYPINETTGYA
LSNNERAAAFAGMSKATWSRHQMSD
YINFILNNMSLNAARAARAKIQLVLGYSEPT"
gene      complement(575616..5773 /locus-tag="Psc-0468"
16)
CDS       complement(575616..5773 /locus-tag="Psc-0468"
16)

/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAZ18331.1"
/db-xref="GI:71038023"
/translation="MQGKQHSDFNDLAAASGLNE
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TTDAPIQHNGNVPADVEQEMRLANMIKRYAQIT
DIGKIVNKVYDTEQKIEYTKTQFA
NEIGNKKLAARNWETKHKRIKSEVAKDLDMMA
VEAQSMFQRYFLIYGTKEVDDVE
RIRLPVDTIKLARPNEYEILWKSEARITIKADNI
WFDPTRTKSPKHKDKDIAINTFDGL
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EWVLRWLAIPLQQEGTKLDALIF
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SSYNDWVSKLYALFEEIFSGNDS
HSQMGVWKQLITGNTIYISKKFMSSGWQDNFVNA
VFLSNNMKPLSLQNDRRHVVCYP
QKKIPEPILNDVATALIDADAKMLRAFYTLMLT
DLKDQTAHTPAIITASKNQLIRLS
QPNWEVFYDDWVKEEFDIPYCSCLSTDLYFVYRN
WCHNRGERPTTETKVMYTIIGRHH
KTRLKYKTPNMMSAKQSTIIAINMPHEHPGSKCS
TQQDWLGSHIQKFKSAINATYDPK"
gene      complement(577513..5785 /locus-tag="Psc-0469"
29)
CDS       complement(577513..5785 /locus-tag="Psc-0469"
29)

/note="Within putative prophage."
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/transl-table=11
/product="possible bacteriophage
DNA primase"
/protein-id="AAZ18332.1"
/db-xref="GI:71038024"
/translation="MSDKRTPLDFEAIRAGAVGN
YVSTIFPAAGIAFSKPAHQHQAC
MCGGSNRFRCDDKRGEGTWICSQCGAGNGFLVK
EFTGLDVHETNKLIAAGIGLDASS
EVTDEQRIQWQSQVVEREAVEKAEKRQARIDAAS
RAQSIWDNAKPAADDPYLLRKNV
SAIGLSQDANDNLIIPMYHNAADKQKITLVNVQT
IAPDSDKLFLKGGGLVSGAYFTIGS
PAMFSAGIILICEGYATGATVFDAMSYSLPVIVA
FNAHNLIPVTQSIRAQYDPHRIII
CADDDSATAIKMRDKDIAAGKEPKPLVEYNAGIR

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gene complement(578519..579022) DAKLAALAVNGELVVPSFDMSDID KDAA
/locus-tag="Psyc-0470"

CDS complement(578519..579022) /locus-tag="Psyc-0470"

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/product="hypothetical protein"
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YNTAALQVNPNRISHTCPPLIEQLLNAAPNSGL
IMDAICCAHGRAGWFLLPDPNDES
EIMTDIGELGRKSADALAIILQAYADGIITPDEF
KAMEKVAHALMSQVQTIMEIAKRd MEKNNVR"

gene complement(579064..579318) /locus-tag="Psyc-0471"

CDS complement(579064..579318) /locus-tag="Psyc-0471"

/note="Part of a putative
prophage"
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/transl-table=11
/product="conserved hypothetical
protein"
/protein-id="AAZ18334.1"
/db-xref="GI:71038026"
/translation="MSSKTIITPKQALAKAVKKAG
GQTELANLIGTKQNVVQWLNRDg
KASARYVSKISEKTNIPSYLERPDIFPAPANDPS
NQQLA"

gene 579446..580120 /locus-tag="Psyc-0472"

CDS 579446..580120 /locus-tag="Psyc-0472"

/note="in putative prophage; helix
turn helix motif"
/codon-start=1
/transl-table=11
/product="possible transcriptional
regulator, Cro/C1 family"
/protein-id="AAZ18335.1"
/db-xref="GI:71038027"
/translation="MALGHRVKEAREFRSLKQGE
LAELIGWTQALSTLENRDSKKSS
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KLIKYPVVKGSAQMGDNGFWSELD
YMGAGGDGYLEVNNASDSAYVIRAVGDSMFPAIR
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gene 580383..580658 /locus-tag="Psyc-0473"

CDS 580383..580658 /locus-tag="Psyc-0473"

/note="Within putative prophage."
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gene 580655..581611 /locus-tag="Psyc-0474"

CDS 580655..581611 /locus-tag="Psyc-0474"

/note="Within putative prophage."
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/transl-table=11
/product="hypothetical protein"
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/db-xref="GI:71038029"
/translation="MSQLISTFQIRFDDETKAEI
GELKNKLDEVNKNLSARDSGLWSE"

gene	581604..581957	SKKKSNSRIGQIIAGAISNQIKEMSRPDGLLKT QADAANDAPHALKQMGQWVFEQ DEKYQSAAVDGDGRAFLYQYKKSALRLGEAKRYF IDSGCDMHQIDGVFDITDWQDSAI DRETIVNDVDYLSSEVPTIQMGSEASYIIVDELQSA LLSKSVPTITQADMPLIFIKNLS VLIQRMHSMDFREDDYAIGGDKLIAWDIVDRN AKIGFLTALNEEKTNFTFCFLSQD TWLLQNTVSVSYSATSNVRNREVRTITEDQLPAFR AALEACYA"
CDS	581604..581957	/locus-tag="Psc-0475" /locus-tag="Psc-0475" /note="Within putative prophage" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18338.1" /db-xref="GI:71038030" /translation="MRNIANIKPSAILVSLIQSA KLSNTVSRIALRDANIQWRAHISK PSQLRDQQTMLDVAAQLRLIIRQVSQKQCGIKRM SWSTLVYLEADLRSAIYAQNINLEP LLDIVAANSEHSEVA"
gene	581957..582475	/locus-tag="Psc-0476" /locus-tag="Psc-0476" /note="Within putative prophage, signal peptide predicted.; Signal predicted by SignalP 2.0 HMM (Signal peptide probability 0.726) with cleavage site probability 0.717 at residue 27"
CDS	581957..582475	/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18339.1" /db-xref="GI:71038031" /translation="MSISKRSKSGPLINVSAAH IGVTTACDRVQRCLNAQGILTDVL SLERSIDVNMDDYVLGNMHLDVILFDKHRNT DSAIKRLIQLWEEGITPDISI LLTCSLANIYQVVSQRSDKHKKVAQHETYLITDK VHYGTRNHVVEITDGKNGQLYAA TIKSLILRELTR"
gene	582890..583405	/locus-tag="Psc-0477" /locus-tag="Psc-0477" /note="Within putative prophage, contains ATP/GTP-binding site motif A."
CDS	582890..583405	/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAZ18340.1" /db-xref="GI:71038032" /translation="MSIKNIEKQPVILNAQEVRA ILHGGKTQHRSVIIPKVEGVGLRF IDYKGGWKAYETDDSDTLTSPDDLLVKCPYGA VGLDNLQGASSGRMIRLGLKITAIR IEQLQDISHKDAEAGVNHFDIEAPLRDQPLSVA QIVFSSHWDAKQLDDDTGWDSNFW VWVIEFEEVAD"
gene	583405..583605	/locus-tag="Psc-0478" /locus-tag="Psc-0478" /codon-start=1 /transl-table=11 /product="possible phage TraR/DksA family protein"
CDS	583405..583605	/protein-id="AAZ18341.1" /db-xref="GI:71038033" /translation="MADDADRANDYVDLTMAHCL SRAPKFDKPSLTCMECEGDIPAK RQAMGGVTLCDVCSVFEGRGK"
gene	584020..585093	/locus-tag="Psc-0479"

CDS 584020..585093 /locus-tag="Psync-0479"
/function="Members of this family cleave DNA substrates by a series of staggered cuts, during which the protein becomes covalently linked to the DNA through a catalytic tyrosine residue at the carboxy end of the alignment."
/note="Within putative prophage."
/codon-start=1
/transl-table=11
/product="possible phage integrase"
/protein-id="AAZ18342.1"
/db-xref="GI:71038034"
/translation="MWHKKRRWQITLEKLPATDRG
YTTASVIRNRLADHAKWGILTIEDI
INELCGNDDAPKTTPTFLDYARLYLKQSDVSKAT
LREYAKSLDRYWIPWPYQREIHTI
TAKEVRTLIADIWSSSEKTRNNNLIPLRGVFGIA
LDDSVIHTNPVDKIKNTKHQSPPP
DPFSRDEMERLLTWLHDKHGKDEAVYWLYFELAF
WTGMRTGELLALTWDDIDWDAGLI
KVSQVMSDGLVNRKTAEYRDVFFNARSEDALK
RLKRIKSAVSDRLFMSPRFINSAW
QTDKTPRRALTEAMKATGIRHRATYTTTRHTFITN
CLTDGLNIYFVAKQTGHVSVRTLET
RYARWIDVSKARSEIAKLNTGSR"

gene complement(585389..585465) /locus-tag="Psync-R0017"

tRNA complement(585389..585465) /locus-tag="Psync-R0017"
/product="tRNA-Pro"

gene complement(585580..587109) /gene="gatB"

CDS complement(585580..587109) /locus-tag="Psync-0480"
/gene="gatB"
/locus-tag="Psync-0480"
/EC-number="6.3.5.-"
/function="This enzyme functions as an alternative to a direct Gln-tRNA synthetase (Gln--tRNA ligase) in mitochondria, chloroplasts, gram-positive bacteria, cyanobacteria, and the Archaea."
/codon-start=1
/transl-table=11
/product="aspartyl-glutamyl-tRNA (Asn/Gln) amidotransferase subunit B"
/protein-id="AAZ18343.1"
/db-xref="GI:71038035"
/translation="MNTAPITDNNAVRKHDVRLPEFVGVGEVYIGIEIHCQLNTESKI
FSSAPITDFGHEPNTQASIVDLGLPGVLPVLNAGV
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NYFYDPLPKGYQITQMANPIVGEYIDVVVNEGE
KNEYPKRMGITRAHLEEDAGKSVH
DAVDGMTGVLDLNRAGTPLIEIVSEPDMSRAHEAL
AYIKAIHQLVTLWGISDAIMAEGS
FRCDNVSIRKPGAELGTRTELKLNLSFRFIERA
INREIERQIDILEDGKVVQATML
YDPERDETRVMRTKEDANDYRYFPDPLLPRVIE
QLTVDSIRAAMPPELPVARRARFEE
ALGLSEYDARILTGSRQIADYFEDVVAEIDQQDA
KMAANWVMGDLGLALNKDDKDIID
SPISAKQLAGMLARIKDDTLSGKLAKKVFGALYE
RAGGDADDAADKIIIEKGLKQETD
TGAIKAIVEEVIKNTAMVEEYRGGKEKAFNGLV
GQVMKASRGSANPQQVNQILKELL D"

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05)
CDS       complement(587109..5886 /locus-tag="Psc-0481"
05)       /gene="gata"
          /locus-tag="Psc-0481"
          /EC-number="6.3.5.-"
          /codon-start=1
          /transl-table=11
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sn/Gln) amidotransferase subunit
A"
          /protein-id="AAZ18344.1"
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          /translation="MSELHLLSTQQLITGLQDKQ
FSSLELTDHYIKRINALDSKINSF
IIHTSETARTQAKAADMVRQGDQRPLLGVPMAH
KDIFCTQGVLTTCGSKMLHNFISP
YDATIVTINIDKAGMISLGKLNMDDEFAMGSDNESS
YYGAVHNPWNIGHVPGSSGGSA
AVAAGVFPVATGSDTGGSIROPASFCLIGIKPT
YGRVSRFGMIAYASSLDQAGSMGR
SAMDCAYLLQPMIGHDPRDATSIKYDMPDYVQDL
NDAAASAGDKPFAGLRIGVAKEYF
SKGLDTEVEQAARAALKKYEELGATIVEVTITDP
EITLATYYMLAPAEASSNLSRFDG
VRFGYRCENPKDLIDLYTRSRSEGFGEVQRRIL
SGTYALSAGYFDAYYIKAQKVRRL
IVKDFEDAFANCVDIASPTAPTAAAYKLGEDLDPA
TMYLGDVYITGVNLAGLPALSPQV
GLTSAGLPIGLQIGQYWQESKLLSTAHLFQQHT
DHLQHSTIAKETV"
gene      complement(588671..5889 /gene="gatC"
85)
CDS       complement(588671..5889 /locus-tag="Psc-0482"
85)       /gene="gatC"
          /locus-tag="Psc-0482"
          /EC-number="6.3.5.-"
          /codon-start=1
          /transl-table=11
          /product="aspartyl/glutamyl-tRNA(A
sn/Gln) amidotransferase subunit
C"
          /protein-id="AAZ18345.1"
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          /translation="MSQQPLTSDNTVSRREEILEV
ANLARLGVDENTADSYAADITKIL
KLMNTLGNVDTTDIKPLSNIHEACQDLRADVAKH
DINRERNQSVAPAVEDGLYLPQV IE"
gene      589699..590727
          /gene="mreB"
          /locus-tag="Psc-0483"

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=> log h
COST IN U.S. DOLLARS
FULL ESTIMATED COST

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SINCE FILE    TOTAL
ENTRY        SESSION
184.40       192.54

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SESSION WILL BE HELD FOR 120 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 09:45:35 ON 12 MAR 2009

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